

CGGACGCGTGGGTGCGAGGCCAAGGTGACCGGGGACCGAGACATTTAGATCTGCTCGGTAGACCTGGTGACACCACCTC**ATG**TTGGCTGCAAGGCTGGTGTGCTCCGGACACTACCTTTCTAGGTTTCCACCCAGCTTCCCAAGGCTCCCTCTTGTGAAGAATTCATCACGAAGAATCATATGGCTGTTTAAACCTAGCAGGGAATATGCCACCAAAACAAGAATTGGGATCCGGCGTGGGA GAACCTGGCCAAAGAATCAAAGAGGCGAGCATTTGAACCATCATGAGAAAAATATTTAAAAATTCATCAGATGGGAAGATGTTTGTGGCTGGAGGGCTGCTGTTGGCTTGGAGCATTTGGTGCTGCTATGTCATGCTGGGATGTCTTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCTCAGTATGTCAAAGGATAGAAATTCATCCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACAGCTTTGTCTGCCATGCACATCAGCAGAACCGCTGTTCATGAATTCATGATCAGAGGCTCTGTGGTGACAATTTGGTGACCTTTGCAGCCATGTTGGAGCTGGAATGCTGGTACGATCAATACCATATGACCAGAGCCGAGCCCAAGACATCTTGCTGGTTGCTACATCTTGGTGTGATGGGTGCGATGGTGGGCTCCTCTGCACAAATATTAGGGGGTCCCTCTTCTCATCAGAGCTGCATGGTACACAGCTGGCAATTTGGTGGAGGCTCTCCTGTCATGTGGCCATGTGTGCGCCACAGTGAAAAGTTTCTGACATGGGTGCACCCCTGGGAGTGGCGCTGGGTCTCGTCTTTGTGTCCTCATTTGGGATCTGATTTCTTCCACCTACCCCGTGGCTGGTGCCACTCTTTTACTCAGTGGCAATGTACGGTGGATTAGTTCTTTTCAAGTATGTTCTCTGTAATGATACCCGAAGAATATCAAGCGTGCAGAAGTATACCCAATGTATGGAGTTCAAAAATATGATCCCATTAACTCGATGTGAGTATCTACATGGATACATAAATATATTTATGCGAGTTGCAACTATGCTGGCACTGGAGGCAACAGAAAAGAA**TG**AGTGACTCAGCTTCTGGCTTCTCTGCTACATCAAAATCTTTGTTAAATGGGCGAGATATGCAATTAATAGTTTGTACAAGCAGCTTTCGTTGAAGTTTAGAAGATAAGAAACATGTCATCATA TTTAAATGTTCCGTAATGTGATGCCCTCAGGCTGCCTTTTTTCTGGAGAATAAATGCAGTAAATCCTCTCCCAATAAGCACACACATTTCAATTCATGTTTGAAGTATTTTAAATGTTTGGTGAATGTGAAACTAAAGTTTGTGTTCATGAGAATGTAAGTCTTTTCTACTTTAAAA TTTAGTAGGTTCACTGAGTAACATAAAATTTAGCAAACTGTGTTTGCATATTTTTTGGAGTGCAGAAATATTGAATATGTATAAGTGATTTGGAGCTTTTGGAGCTTTTGAAGGACACAGAGAAGGAGTGACCTCGCAATCTTTGTTTTTAAATACTTAGCACTTAGCACTTTGTGTTATTGATTA GTGAGGAGCCAGTAAGAAACATCTGGGTATTGGAACAAAGTGTCATGTTGATCACTTTCAATTTGCTGAACTTAAACAACTGTTCACTCTGAAACAGGCACAGGTGATGCATCTCTGCTGTGCTTCTCAGTGCTCTCTTCCAATATAGATGTGGTTCATGTTTGACTTGTACAGAATGTTAATCATACAGAAATCCTTGTGAATGTAATATGTTGTTTCACTTTTGAATGTTACAAAAGGAATAAATCTTAAACTATTTCTCAAGAGAAAATATTCAAAGCATGAAATATGTTGCTTTTCCGAAATAACAACAGTATACTCATG

**FIGURE 2**

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KEAALEPSMEKIFKIDQMGRWFVAGGAAVGLGALCYYGGLSNEIGAIEKAVIWPQYVKDRI  
HSTYMYLAGSIGLTALSAIAISRTPVLMNFMMRGSWVTIGVTFAAMVGAGMLVRSIPYDQSP  
GPKHLAWLLHSGVMGAVVAPLTLGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL  
GVGLGLVFVSSLGSMFLPPTTVAGATLYSVAMYGGLVLFMFLLYDTQKVIKRAEVSPMYGV  
QKYDPINSMLSIYMDTLNIFMRVATMLATGGNRKK

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**FIGURE 3**

GAAGGCTGCCTCGCTGGTCCGAATTCGGTGGCGCCACGTCCGCCCGCTCTCCGCCCTTCTGCAT  
CGCGGGCTTCGGGGGCTTCCACCTAGACACCTAACAGTCCGGAGCCGGCGCGTCTGTGAGGG  
GGTCGGCACGGGGAGTCGGGCGGTCTTGTGCATCTTGGCTAGCTGTGGGTGCAAG**ATG**TCGG  
ACATCGGAGACTGGTTTCAGGAGCATCCCGGCGATCACGCGCTATTGGTTCGCCGCCACCCTC  
GCCGTGCCCTTGGTCGGCAAACTCGGCCTCATCAGCCCGGCCCTACCTCTTCCCTCTGGCCCCGA  
AGCCTTCCCTTTATCGCTTTTCAGATTGGAGGGCAATCACTGCCACCTTTTATTTCCCTGTGG  
GTCCAGGAACCTGGATTCTTTTATTGGTCAATTATATTTCTTATATCAGTATTCTACGCCGA  
CTTGAAACAGGAGCTTTTGATGGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTTAACTG  
GATTTGCATCGTGATTACTGGCTTAGCAATGGATATGCAGTTGCTGATGATTCCCTCTGATCA  
TGTCAGTACTTTATGCTGGGCCAGCTGAACAGAGACATGATTGTATCATTTTGGTTTGGGA  
ACACGATTTAAGGCCTGCTATTACCCTGGGTATCCTTGGATTCAACTATATCATCGGAGG  
CTCGGTAATCAATGAGCTTATTGGAAATCTGGTTGGACATCTTTATTTTTTCTTAATGTTCA  
GATACCAATGGACTTTGGGAGGAAGAAATTTTCTATCCACACCTCAGTTTGTGACCGTGG  
GTGCCCAGTAGGAGAGGAGGATATCAGGATTTGGTGTGCCCCCTGCTAGCATGAGGCGAGC  
TGCTGATCAGAATGGCGGAGGCGGGAGACACAACCTGGGGCCAGGGCTTCGACTTGGAGACC  
AG**TGA**AGGGGCGCGCTCGGGGAGCCGCTCCTCTCAAGCCACATTTTCCCTCCAGTGTGGGTG  
CAGCTTAACAACCTGCGTTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTCTTT  
AGTACGAGACAAGATTCTTAAATCCCGAAGAAAAATATAAGTGTTCACAAGTTTCACGAT  
TCTCATTTCAAGTCTTACTGCTGTGAAGAACAATAACCAACTGCTGCAAAATGGCAAACTGAC  
TACATTTTTTGGTGTCTTCTCTTCTCCCTTTTCCGTCTGAATAATGGGTTTTAGCGGGTCCCT  
AATCTGCTGGCATTGAGCTGGGGCTGGGTCAACAAACCCCTCCCAAAAGGACCTTATCTCTT  
TCTTGCACACATGCCCTCTCTCCCACTTTTCCCAACCCCACTTTGCAACTAGAAAAAGTTG  
CCCATAAAAATTGCTCTGCCCTTGACAGGTTCTGTTATTTTATGACTTTTGCCAAAGGCTGGT  
ACAACAATCATATTACGCTTATTTTCCCTTTTGGTGGCAGAACTGTTACCAATAGGGGGAG  
AAGACAGCCACGGATGAAGCGTTTTCTCAGCTTTTGGAAATGCTTCGACTGACATCCGTTGTT  
AACCCTTTTGCCACTCTTCAGATATTTTTTATAAAAAAGTACCACCTGAGTTTCATGAGGCCA  
CAGATTGGTTATTAATGAGATACGAGGGTTGGTGTCTGGGTGTTTGTTCCTGAGCTAAGTGA  
TCAAGACTGTAGTGGAGTTGCAGTTAACATGGGTTAGGTTAAACCATGGGGGATGCACCCC  
TTTGCCTTTCATATGTAGCCCTACTGGCTTGTGTAGCTGGAGTAGTTGGGTTGCTTTGTGT  
TAGGAGGATCCAGATCATGTTGGCTACAGGAGATGCTCTCTTTGAGAGGTCCTGGGCATTG  
ATTCCCATTTCAATCTCATTTCTGGATATGTGTTCAATTGAGTAAAGGAGGAGAGACCCCTATA  
CGCTATTTAAATGTCACTTTTGTGCTATCCCCGTTTTTTGGTCAATGTTTCAATTAAATTGT  
GAGGAAGCGCAGCTCCTCTCTGCACGTAGATCATTTTTTAAAGCTAATGTAAGCACATCTA  
AGGGAAATAACATGATTTAAGGTTGAATGGCTTTAGAATCATTTGGGTTTGGAGGGTGTGTTA  
TTTTGAGTCATGAATGTACAGAGCTCTGTAATCAGACCAGCTTAAATACCCACACCTTTTTT  
TCGTAGGTGGGCTTTTCCCTATCAGAGCTTGGCTCATAACCAATAAAGTTTTTGAAGGCCA  
TGGCTTTTACACAGTTATTTTATTTATGACGTTATCTGAAAGCAGACTGTTAGGAGCAGT  
ATTGAGTGGCTGTCACTATTTGAGGCAACTAAAAGGCTTCAAACGTTTTGATCAGTTTCTT  
TTCAGGAACATTTGCTCTAACAGTATGACTATTCTTCCCCACCTCTTAAACAGTGTGAT  
GTGTGTTATCTAGGAAATGAGAGTTGGCAAACAACCTTCTCATTTTGAATAGAGTTTGTGTG  
TACTTCTCCATATTTAATTTATATGATAAAATAGGTGGGGAGAGCTGAACCTTAACCTGTCA  
TGTTTTGTGTTTCATCTGTGGCCACAATAAAGTTTACTTTTAAAAATTTAGAGGCCATTACT  
CCAATTATGTTGCACGTACACTCATTGTACAGGCGTGGAGACTCATTTGTATGTATAAGAATA  
TTTTCTGACAGTGAGTGACCCGGAGTCTCTGGTGTACCCCTTACCAGTCAGCTGCCGTCCGAG  
CAGTCATTTTTTCCATAAAGGTTTACAAGTATTTAGAAGTTTTCAGTTGAGGCAAGTAAAGTTC  
ATGAAGTTATTCCTCTTAAACATGTTAGGAAGCTGATGAGTTATTGATTTGTCTGGATT  
ATGTTTCTGGAATAATTTTACCAAAACAGCTATTGAGTTTTGTGCTTGAAGGCAAAACA  
TGACAGTGGATTCTCTTTACAAATGGAAAAAAATCCTTATTTTGTATTAAGGACTTCCC  
TTTTTGTAAACTAATCCTTTTTTATGGTAAAAATTGTAATTAATATGTCACACTTG

**FIGURE 4**

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGILSPAYLFLWPEAFLYRFQIWRPITATFYF  
PVGPGTGFLYLVNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP  
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIIGGSVINELIGNLVGHLYFFL  
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWQGFR  
LDQ

**Transmembrane domain:**

amino acids 98-116, 152-172

**N-myristoylation site.**

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

**Glycosaminoglycan attachment site.**

amino acids 218-222

**FIGURE 5**

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAACCTGGTTG  
 GTAGCTTCTATCCTGCGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCTACTCCCTCTCGGCT  
 CCTTGTGGCCCAAAGGCTAACC GGGTCCGGCGGTCTGGCCTAGGGATCTTCCCGTTGCC  
 CCTTTGGGGCGGG**ATG**GCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG  
 CGGGGTTCTGCGAGGCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT  
 GAAGTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCAGAGCCGGTGATTTTGGT  
 GGCCTGTGTTCCCCTTGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC  
 ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTAGAAGGTTACCTCAAAGAAATTGGAATT  
 AATGAAGATCAATTTCAAGAAGCATGCACCTTCTCCTCTTGCAAAGACCCATACATCACAGGC  
 CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA  
 AAAACATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAAGAGAGAAATGGTGTATTACCT  
 GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTGAAACACGAAGAGATGAAAATCCT  
 GAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAAA  
 AACAGTTATCAGAGGCTAAAACAGAAGAGCCACAGTGCATTCCAGTGAAGCTGCAATAATG  
 AATAATTCCCAAGGGGATGGTGAACATTTTGCACACCCACCCTCAGAAGTTAAAATGCATTT  
 TGCTAATCAGTCAATAGAACCCTTGGGAAGAAAAGTGGAAAGGTCTGAAACTTCCTCCCTCC  
 CACAAAAAGGCCTGAAGATTCTTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC  
 TTATCAGTACTTGGAACAGAAGAACTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA  
 TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG  
 GAAAACCCACTGGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAG  
 CAAACATTACTAAAGAGGAGATTGCTTGCAAGAGAACTCAAAGAAGAAGTTATTAATAAG**TA**  
**A**TAATTAAGACAATTTAACAAAATGGAAGTTCAAATTGTCTTAAAAATAAATTATTTAGTC  
 CTTACACTG

**FIGURE 6**

MAAEEEEDEVWVVESIAGFLRGPDWSIPILDFVEQKCEVNCKGGHVITPGSPEPVILVACVP  
LVFDDEEESKLTYTEIHQEYKELVEKLLLEGYLKEIGINEDQFQEACTIONSPAKTHTSQAILQP  
VLAEDFTIFKAMMVQKNIEMQLQAIRIIQERNGLPDCLTDGSDVVSDEHEEMKILREVL  
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS  
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPANLSVLGTEELRQREHYLKQKRDKILMS  
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEEKQTLLKRLLAEKLKEEVINK

**N-glycosylation sites.**

amino acids 224-228, 246-250, 285-289

**N-myristoylation site.**

amino acids 273-279

**Amidation site.**

amino acids 252-256

**Cytosolic fatty-acid binding proteins.**

amino acids 78-108

**FIGURE 7**

GGGCACAGCACATGTGAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT  
TCATCAGGAATACAAAGAAGTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA  
TTAATGAAGATCAATTTCAAGAAGCATGCACCTTCTCCTCTTGCAAAGACCCATACATCACAG  
GCCATTTTGCACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC  
AGAAAAACATTGAAATGCAGCTGCAAGCCATTCCAATAATTCAAGAGAGAAATGGTGTATTA  
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAT  
CCTGAGGGAAGTTCTTAGAAAATCAAAAGAGGAATATGACCAGGAA

**FIGURE 8**

GCGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTG  
 TAGCTTCTCCAGTATGGACCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG  
 TCTCAGCTCTAGGATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTA AAAAAC  
 AGTGGAA**ATG**GAAAAACAGTGCCTGAGTCATCCTGTAATATGCTCCTTGTCACAAATGTATAC  
 ATTCTGTCTAGGTGCCATATTATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATT  
 CTGCCAATGAAGAAAAAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAACTG  
 GTGAAGCTAGTTTTCTGTGTGCTTGTGTCTATTCTGTGTTATAAAGAAAGATCATCAAAGTAG  
 AAATTTGAAATATGCTTCCTGGAAGGAATTCTCTGATTCATGAAGTGGTCCATTCTCGCCT  
 TTCTTTATTTCTGGATAACTTGATTGTCTTCTATGTCTGTCTATCTTCAACCAGCCATG  
 GCTGTTATCTTCTCAAATTTTAGCATATAACAACAGCTCTTCTATTAGGATAGTGTGAA  
 GAGCGCTCTAACTGGATCCAGTGGGCTTCCCTCCTGACTTTTTTTGTCTATTGTGGCCT  
 TGACTGCCGGGACTAAAACTTTACAGCACAACCTGGCAGGACGTGGATTTCATCAGATGCC  
 TTTTTCAGCCCTTCCAATTCCTGCCTTCTTTTCAGAAAGTGAGTGTCCAGAAAAGACAATTG  
 TACAGCAAAGGAATGGACTTTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTCACTC  
 ACATCCGCTCTTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTTTTATTTCTTCAATGGCT  
 AATATCTATAATGAAAAGATACTGAAGGAGGGGAACCAAGCTCACTGAAAGCATCTTCATACA  
 GAACAGCAAACCTCTATTTCTTTGGCATTCTGTTTAATGGGCTGACTCTGGGCCCTTCAGAGGA  
 GTAACCGTGATCAGATTAAAGAACTGTGGATTTTTTTATGGCCACAGTCATTTTCAGTAGCC  
 CTTATTTTTGTAACCTGCATTCCAGGGCCTTTCACTGGCTTTTCACTCTGAAGTTCTCTGGATAA  
 CATGTTCCATGTCTTGATGGCCAGGTTACCACTGTCTATTATCACAACAGTGTCTGTCTGG  
 TCTTTGACTTTCAGGCCCTCCCTGGAATTTTTCTTGAAGCCCATCAGTCTCTTCTCTCTATA  
 TTTATTTATAATGCCAGCAAGCCTCAAGTTCGGAATACGCACCTAGGCAAGAAAGGATCCG  
 AGATCTAAGTGGCAATCTTTGGGAGCGTTCCAGTGGGGATGGAGAAGAACTAGAAAGACTTA  
 CAAACCCCAAGAGTGATGAGTCAGATGAAGATACTTTCT**TAAC**TGGTACCCACATAGTTTGCA  
 GCTCTCTTGAACCTTATTTTCACATTTTCAGTGTTTGTAATATTTATCTTTTCATCTTGATA  
 AACCAGAAATGTTTCTAAATCCTAATATCTTTGCATATATCTAGCTACTCCCTAAATGGTT  
 CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATTTCTAAGAACTGATACAGGAGTAACA  
 ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT  
 TTTCTTGGCCTTCAAGCTTCCAAAAAAGCTGTAATAATCATGTTAGCTATAGCTTGTATAT  
 ACACATAGAGATCAATTTGCCAAATATTCACAATCATGATGTTCTAGTTTACATGCCAAAGT  
 CTCCCTTTTTTAACATTATAAAAGCTAGGTTGTCTCTGAAATTTGAGGCCCTAGAGATAGT  
 CATTTTGCAAGTAAAGAGCAACGGGACCCCTTTCTAAAAACGTTGGTTGAAGGACCTAAATAC  
 CTGGCCATACCATAGATTTGGGATGATGATGCTGTGCTAAATATTTTGTCTGAAGAAGCAGT  
 TTCTCAGACACAACATCTCAGAATTTTAATTTTTAGAAATTCATGGGAAATTTGGATTTTGT  
 AATAATCTTTTGATGTTTTAAACATTGGTTCCCTAGTCACCATAGTTACCACCTTGATTTTTA  
 AGTCATTTAAACAAGCCACGGTGGGGCTTTTTCTCCTCAGTTTGAGGAGAAAAATCTTGAT  
 GTCATTACTCTGAATTATACATTTTGGAGAATAAGAGGGCATTATTTTATTAGTTTACT  
 AATTCAAGCTGTGACTATTGTATATCTTTCCAAGAGTTGAAATGCTGGCTTCAGAATCATAC  
 CAGATTGTGATGAAGCTGATGCCTAGGAACTTTTAAAGGGATCCTTTCAAAGGATCACTT  
 AGCAAACACATGTTGACTTTTAACTGATGTATGAATATTAATACTCTAAAAATAGAAAGACC  
 AGTAATATATAAGTCACTTTACAGTGTCTACTTCACACTTAAAAGTGCATGGTATTTTTCATG  
 GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTAA  
 AAATTAGCAAACAAAAGTGACTTGCTCAGGGTCACTGCAGCTGGGTGATGATAGAAGAGTGGG  
 CTTTAACTGGCAGGCCTGTATGTTTACAGACTACCATACTGTAATAATGAGCTTTATGGTGT  
 CATTCTCAGAACTTATACATTTCTGCTCTCCTTTCTCCTAAGTTTTCATGCAGATGAATATA  
 AGGTAATATACTATATATAATTCAATTTGTGATATCCACAATAATATGACTGGCAAGAATTG  
 GTGGAAATTTGTAATTAATAAATTATTAAACCT



**FIGURE 9**

MEKQCCSHPVICSLSTMYTFLLGAI FIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK  
 LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLPAMAV  
 IFSNFSIITTALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHD AFF  
 SPSNSCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI  
 YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSAFSVALI  
 FVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFI  
 YNASKPQVPEYAPRQERIRDLSGNLWERSSSGDGEELERLTKPKSDESEDEDTF

**Transmembrane domains:**

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,  
 298-318, 328-368

**N-glycosylation sites.**

amino acids 128-132, 204-208, 218-222, 374-378

**Glycosaminoglycan attachment site.**

amino acids 402-406

**N-myristoylation sites.**

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

**FIGURE 10**

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTCCCCAATCCGGACGTAATCGTGGTTTTTG  
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC  
GTATGGACCCATAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG  
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTA AAAAACAGTGAATGGAA  
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCACAATGTATACATTCTGCTAGG  
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG  
AAAACAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT  
TTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA  
TGCTTCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCTGCCTTTCTTTATTTCC  
TGGATAACTTGATTGTCTTCTATGTCCTGTCCTATCTTCAACCAGCCATGGCTGTTATCTTC  
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTCAGGATAGTGCTGAAGAGGCGCTAAA  
CTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTTGTCTATTGTGGCCTTGACTGCCGGGA  
CTAAAACTTTA

**FIGURE 11**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGCCGGCTTGGCTAGCGCGCGGGCGGC  
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGCCTGCGGGGACAGAGGAGCAT  
 CCGGCTACACAGGTCCCAAGCGGCGTGGCCCGCGGGTCATGGCCAAAGGAGAAGGCGCCGAG  
 AGCGGCTCCGCGGCGGGGCTGCTACCCACCAGCATCCTCCAAAGCACTGAACGCCCGGCCCA  
 GGTGAAGAAAGAACCAGAAAAGAAGAAACAACAGTTGTCTGTTTGAACAAGCTTTGCTATG  
 CACTTGGGGGAGCCCCCTACAGGTGACGGGCTGTGCCCTGGGTTTCTTCCTTCAGATCTAC  
 CTATTGG**ATG**TGGCTCAGGTGGGCCCTTTCTCTGCCCTCCATCATCTGTTTGTGGGCGGAGC  
 CTGGGATGCCATCACAGACCCCTGGTGGGCCTCTGCATCAGCAAATCCCCCTGGACCTGCC  
 TGGGTGCGCTTATGCCCTGGATCATCTTCTCCACGCCCCTGGCCGTCAATTGCCCTACTTCCCTC  
 ATCTGGTTCGTGCCCGACTTCCCACACGGCCAGACCTATTGGTACCTGCTTTTCTATTGCCT  
 CTTTGAACAATGGTCACGTGTTTCCATGTTCCCTACTCGGCTCTCACCATGTTTCATCAGCA  
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTGCTGGGCAC  
 AGTGCTGGGCACGGCGATCCAGGGACAAATCGTGGGCCAAGCAGACACGCCTTGTTTCCAGG  
 ACTTCAATAGCTCTACAGTAGCTTCACAAAGTGCCAACCATAACATGGCACCCTTCACAC  
 AGGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTG  
 TGCTGTCTATCCTGATCCTGGGCGTGGGGAGCAGAGAGAACCCTATGAAGCCAGCAGTCTG  
 AGCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCAATGAGCCACGGCCCATACATCAAACCTT  
 ATTACTGGCTTCTCTTACCTCCTTGGCTTTCATGCTGGTGGAGGGAACTTGTCTTGTT  
 TTGCACCTACACCTTGGGCTTCCGCAATGAATTCAGAATCTACTCCTGGCCATCATGCTCT  
 CGGCCACTTTAACCATTCCCATCTGGCAGTGGTTCCTTGACCCGGTTTGGCAAGAAGACAGCT  
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA  
 CCTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTAC  
 TACCTTGGTCCATGCTGCCTGATGTATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT  
 GGAACCGAGGCCATCTTCTTCTCTTCTATGTCTTCTTACCAAGTTTGCCCTCTGGAGTGTC  
 ACTGGGCATTTCTACCCTCAGTCTGGACTTTGCAGGGTACCAGACCCGTGGCTGCTCGCAGC  
 CGGAACGTGTCAAGTTTACACTGAACATGCTCGTGACCATGGCTCCCATAGTTCTCATCCTG  
 CTGGGCCTGCTGCTCTTCAAATGTACCCATTGATGAGGAGAGGCGGCGGAGAATAAGAA  
 GGCCCTGCAGGCACTGAGGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG  
 AGCTGGCTAGCATCCTC**TAG**GGCCCCGCCACGTTGCCCGAAGCCACCATGCAGAAGGCCACAG  
 AAGGGATCAGGACCTGTCTGCCGGCTTGCTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA  
 CTGAAGACTCAAGGAGGTGGCCAGGACACTTGCTGTGCTCACTGTGGGGCCGGCTGCTCTG  
 TGGCCTCCTGCCTCCCCTCTGCCTGCCTGTGGGGCCAAGCCCTGGGGCTGCCACTGTGAATA  
 TGCCAAGGACTGATCGGGCCTAGCCCGGAACACTAATGTAGAAACCTTTTTTTTACAGAGCC  
 TAATTAATAACTTAATGACTGTGACATAGCAATGTGTGTATGTATATGTCTGTGAGCTA  
 TTAATGTTATTAATTTTCATAAAAGCTGGAAGC

MWLRWALSLPSSSCIWAEPMGMSQTPWVASASANPPGPAWVALCPGSSSPRPWPSLPTSSSG  
SCPTSH TARPIGT CFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL  
GTAIQGGIVGQADTPCFQDFNSSTVASQSANHTHTTSHRETQKAYLLAAGVIVCIYIICAV  
ILILGVREQREPYEAQQSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVLFCT  
YTLGFRNEFQNLLLAIMLSATLTIPIWQWFLTRFGKKTAVYVVGISSAVPFLILVALMESNLI  
ITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLG  
ISTLSLDFAGYQTRGCSQPERVKFTLNLMLVTMAPIVLILLGLLLFKMYPIDEERRRQNKAL  
QALRDEASSSGCSETDSTELASIL

**FIGURE 13**

GGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT  
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA  
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA  
TTACTGGCTTCCTCTTCACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTGTCTTGTTT  
TGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCTC  
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG  
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC  
CTCATATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT  
ACCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG  
GAACCGAGCCCAT

**FIGURE 14**

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT  
 ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAAACAGAAAACCTGTAGAAAATGT  
 GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT  
 TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT  
 CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG  
 CAGTTTTATGCATTGCTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA  
 GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGCTACTTGGGAATACTGAGTTGTTTAGG  
 ACTTTCTATTGTGGCAAACCTCCAGAAAAACAACCCTTTTGTGCTGCACATGTAAGTGGAGCTG  
 TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCCTACCAAATG  
 CAGCCCAAAATCCATGGCAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG  
 AGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTTGGGACTG  
 ATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT  
 ACTGCAGCAGAATGGTCTATGTCATTTTCCTTCCTTTGGTTTTTTCCTGACTTACATTCGTGA  
 TTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAACCCTCTATGACACTG  
 CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCAGAGATATTTGATGAAAGGAT  
 AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAGTTGCTTA  
 TTCTTCTCTGAAATTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA  
 ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCATCAAGAAGACTA  
 TTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAGACTATG

**FIGURE 15**

MWWFQQGLSFLPSALVIWTSAAFI<sup>1</sup>FSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI  
AAVLCIATIIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG  
AVLTFGMGSLYMFVQTILSYQM<sup>2</sup>QPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFG  
TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLT<sup>3</sup>YIRDFQKISLRVEANLHGLTLYD  
TAPCPINNERTRLLSRDI

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**FIGURE 16**

CGGACGCTTGGGCNCGGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT  
TCCGTCTCTCGGGTCTTTTCCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA  
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCTCTGGTTTGTGAAGCAGT  
TACCAAGAATCTTCAACCCTTCCCACAAAAGCTAATTGAGTACACGTTCCCTGTTGAGTACA  
CGTTCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA  
GTTGTAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT  
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT  
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC





## **FIGURE 18**

MRPLLGLLLVFAGCTFALYLLSTRLPRGRRLGSTEEAGGRSLWFPSDLAELRESEVLREYR  
KEHQAYVFLFLFCGAYLYKQGFAPGSSFLNLVLAGALFGPWLGLLLCCVLTSVGATCCYLLSS  
IFGKQLVVSYPFDKVALLRKVEENRNSLFFLLFLRLFPMTPNWFLNLSAPILNIPVQFF  
FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKFSQKHLQ  
LNETSTANHIHSRKDT

### **Important features:**

#### **Signal peptide:**

amino acids 1-17

#### **Transmembrane domains:**

amino acids 101-123, 189-211

#### **N-glycosylation sites.**

amino acids 172-176, 250-254

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 240-244, 261-265

#### **N-myristoylation site.**

amino acids 13-19, 104-110, 115-121, 204-210

#### **Amidation site.**

amino acids 27-31

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 4-15

#### **Protein splicing proteins.**

amino acids 25-31

#### **Sugar transport proteins.**

amino acids 162-172

CCGAGGCGGGAGGAGGCCGAGGGGGCGCGAGCCCCGATGAATCATTGTAGTCAATCATTTT  
CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACAGTGGTTTCCGAACGCCAGCTCAGAA  
TAGGAAAATAACTTTGGGATTTTATATTGGAAGACATCGATCTTGTCTGCCAACGAGATCAGCA  
TTTATGACAACTTTTCTCAGAGACTGTTGATTGTTGTTGAGACAGACCGGCCATCAGTGTGCGATG  
TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAAATGAACCTCAGAGACC  
CCCCCGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT  
TGCTCACTGCCTACTTTGTGATTCAACCTTTTACAGCCATTAGCACCTGAGCCAGTGCCTTCT  
GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCTTGCCCATTGCCAA  
GAAGTACATGTCAGAAAATAAGGGAGTTCTCTGCATGGGGGTGATGAAGACAGACCCCTTC  
CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCCTGCC  
AACTGCACCTGGCTGTGCCCGAAGAACCTGAAAGGTGATGCTCTTGAAAGACGCCCCAAGGAA  
ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCTGTTGGAGGAAGAGATTC  
AGCATTTTTTGTGCCAGTACCCTGAGGCACAGAAAGGCTTCTCTGAAGGGTTTTTCGCCAAG  
TGGTGGCGCTGCTTTCTTGAGCGGTGGTTCCCATTTCTCTTATCCATGGAGGAGACCTTGAA  
CAGATCACAAATGTTACGTGAGCTTTTTCTGTTTTCACTCACCTGCCATTTCCAAAAGATG  
CCTCTTTAAACAAGTGCTCCTTTCTTACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG  
ATGCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA  
GTGCCGAAGACATTGTCACTGTGTGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCTG  
ACACCACCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT  
GGAACCGCTTTCTCAGAACTGTAGGAAATAGAACTGTGCACAGGAACAGCTTCCAGAGCCGA  
AAACCAAGTTGAAAGGGGAAAAATAAAAAAAGAAACGATGAAACTGCAAAAA

**FIGURE 20**

MDLAANEISIIYDKLSETVDLVRQGTGHQCGMSEKAIEKFIRQLLEKNEPQRPPPYPLLIVVY  
KVLATLGLILLTAYFVIQPFSPLAPEFVLSGAHTWRSLIHHIRLSLPIAKKYMSENKGVPL  
HGGDEDRPFPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKT  
GKPLLEEEIQHFLCQYPEATEGFSEGGFFAKWWRCFPERWFFFPYPWRRPLNRSQMLRELFV  
FTHLPFPKDASLNKCSFLHPEFVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRRHCSVAMP  
IEPGDIGYVDTHWKVYVIARGVQPLVICDGTAFSEL



**FIGURE 21**

CCACGGTGTCGGTTCTTCGCCCCGGCGGCAGCTGTCCCCGAGGCGGGAGGAGCCCCGAGGGGCG  
CGAGCCCCGCATGAATCATTTGTAGTCAATCATTTTCCAGTTCTCAGCCGTTCAAGTTGTGATC  
AAGGGACACGTGGTTTCCGAAGTCCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT  
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAACTTTCAGAGACTGTTG  
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTTATC  
AGACAGCTGCTGGAAAAGAAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT  
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC  
CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC



**FIGURE 22**

CCCACGCGTCCGCCCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG  
 CAGGCTCCCCACTTGCAGCTGCAGCAGCTGCAGCAGCTGCAGAGCGCTGCTCCTGGCTGGTG  
 CCAGTGGTGCCGACCGTGCTAGACCGTGCCATGAGCCGCTGGGGCTGCAGTGGGGACTGCC  
 CTCCCTGCCACCCACCAATGGCAGCCCCACCTTCTTTGAAGACTTCCAGGCTTTTTGTGCCA  
 CACCCGAATGGCGCCACTTCATCGACAAACAGGTACAGCCAACTGTCAGTTCGAATG  
 GACACGTATGCTAAGAGCCACGACCTTATGTACGGTTCTGGGAATGCCGTGCTATGACATGCT  
 TATGAGCAGTGGGCAGCGGCCAGTGGGAGCGCGCCAGAGTCGTCGGGCCCTCCAGGAGC  
 TGGTGCTGGAACCTGCGCAGAGGCGGGCGCGCTGGAGGGGTACGCTACACGGCAGTGTCTG  
 AAGCAGCAGGCAACGAGCAGCTCCATGGCCCTGCTGCATGGGGGGCGCTGTGGCGCCAGCT  
 CGCCAGCCCATGTGGGGCCTGGGCGCTGAGGGACACTCCCATCCCCGCTGGAACTGTCCA  
 GCGCCGAGACATATTCACGCATGCGTCTGAAGCTGGTGCCCAACCATCACTTCGACCTCAC  
 CTGGAAGCCAGCGCTCTCCGAGACAATCTGGTGAGGTTCCCTGACACCCACCGAGGAGG  
 CTCCTGCTGCTGCGCAGTGACCAAAGAGGCCAAAGTGAGCACCCACCCGAGTTGCTGCAGG  
 AGGACAGCTCGCGCAGGACGAGCTGGCTGGCTGAGCTGGAGACCCGATGGAGGCGCAGCAACTG  
 GATGAGCAGCGTGAGAAGCTGGTCTGTCGGCCGAGTGCCAGCTGGTGACGGTAGTGCCGCT  
 GGTCCCAGGGCTGCTGGAGGTCAACACAGAAATGTACTTCTACGATGGCAGCAGCTGAGC  
 GCGTGGAAACCGAGGAGGCTCGGCTATGATTTCGGGCGCCACTGGCCAGCTGCGTGAG  
 GTCCACCTGCGGCGCTTCAACCTGCGCCGTTTCAGCACTTGAGCTCTTCTTATCGATCAGGC  
 CAACTACTTCTCACTTCCATGCCATGCAAGGTGGGACGACCCAGTCTCATCTCTTAGCCAGA  
 CTCCGAGCCACCGCTGGCCCATCCCAACCCATACCCAGGTACGGAAACGAGTGTATCTCG  
 TGGCTCTGCGCCTACGGCCCCCTCTCAAGGCTACCTAAGCAGCGGCTCCCCAGGAGAT  
 GCTGCGTGCTCAGGCCTTACCCAGAAATGGGTACGCGTGAGATATCCAACCTTCAGTACT  
 TGTGCAACTCAACACCATTCGCGGGCGGACCTACAATGACCTGTCTCAGTACCTGTGTTC  
 CCCTGGTCTGCAAGACTACGTGTCCCCAACCCCTGGACCTCAGCAACCCAGCGCTCTCCG  
 GGACCTGTCTAAGCCCATCGGTGTGTGTGAACCCCAAGCATGCCAGCTCGTGAGGGGAAGT  
 ATGAAAGCTTTGAGGACCCAGCAGGGACCATTGACAAGTTCCACTATGGCACCACCTACTCC  
 AATGACGAGCGCGTGATGCACTACCTCATCCGCGTGAGGACCCCTTACCTCCCTGCACGTCCA  
 GCTGCAAAAGTGGCCGCTTTTGACTGCTCCGACCGGCACTTCCACTCGGTTGCCGCGCAGCTGGC  
 AGGCACGCTGGAGGCCCTGCCGATGTGAAGGAGCTCATCCCGGAATTTCTTACTTCTCTCT  
 GACTTCTGGAGAACCAGAACCGCTTTTGACCTGGGCTGTCTCCAGTGAACACGGAAGGT  
 AGGCGATGTGGTGCTACCCCCGTGGGCCAGCTCTCTTGAGGACTTCATCCAGCAGCACCGCC  
 AGGCTCTGGAGTCGGAGTATGTGCTGACACCTACACGAGTGGATCGACCTCATCTTTGGC  
 TACAAGCAGCGGGGGCCAGCCGCGGAGGAGGCCCTCAATGTCTTCTATTACTGCACCTATGA  
 GGGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATTA  
 TCAGCAACTTTGGGCGAGACTCCCTGTCAGCTGCTGAAGGAGCCACATCCAACCTCGGCTCTCA  
 GCTGAGGAAGCAGCCCATCGCCTTGACGCTGGACACTAATCACTAGCATCTTCCAGCA  
 CCTGGACGAACCTCAAGGCATTTCTTCGAGAGGTGACTGTGAGTGCCAGTGGGCTGCTGGGCA  
 CCCAGAGCTGGTTGCCTATGACCGCAACATAAGCAACTATTCAGCTTCAGCAAAGACCCC  
 ACCATGGGCGACCCACAAGACGACGAGCTGCTGAGTGGCCGCTGGGTGCCAGGCACTGGTGT  
 GAGTGGACAAGCACTGGCAGTGGCCCGGATGGAAGCTGCTATTAGCCGCTGGCCACTGGG  
 ATGGCAGCGTGCGGGTGACTGCATACCCGCTGGCAAGCTGTTGAGCCAGCTCAGCTGCCAC  
 CTTGATGTATTAACCTCCCTTGCACTGGACACCTGTGGCATCTACCTCATCTCAGGCTCCCG  
 GGAACCCAGCTGCATGGTGTGGCGGCTCCTGCATCAGGGTGGTCTGTGAGTAGGCTGGCAG  
 CAAAGCCTGTGCGAGTCTCTGATGGCGATGGGGCTGCAGTGAGCTGTGTGGCCATCAGCACT  
 GAACTTGACATGGCTGTGTCTGGAATGAGGATGGAACATGTATCATACACTGTACGCGC  
 CGGACAGTTTGTAGCGGCATACGGCTCTGGGTGCCACATTCCTTGGACCTATTTTCCACC  
 TGGCATTTGGGTCGGAAGGCCAGATGTGTGTACAGAGCTCAGCGTGGGAACGCTCTGGGGCC  
 CAGGTCACTTACTCTTGCACCTGTATTAGTCAATGGGAAGTTCGGGCTTCACTGCCCT  
 GGCAGAGCAGCCTACAGCCCTGACGCTGACAGAGGACTTTGTGTGCTGGGCACGCCAGT  
 GCGCCTGCACATCTTCAACTAAACACACTGCTCCCGCGCGCTCCCTTGCCTGCAAG  
 GTGGCCATTCGCGAGCTGCGCGTGACCAAGGAGCGCAGCCAGCTGCTGGTGGGCTGGAGGA  
 TGGAAGCTCATCGTGGTGTGTCGCGGGCGACCCCTCTGAGGTGCGCAGCAGCCAGTTTCGCG  
 GGAAGCTGTGGCGGTCTCGCGGCGCATCTCCAGGTGTCTCGGAGAGAGCGGAATACAAC  
 CCTACTGAGGCGCGCTGAACCTGGCCAGTCCGGCTGCTCGGGCCCCGCCCCGGCAGCCGCT  
 GCCCGGGAGGCCGCCCAAGAGTGGCGGGGAACACCCCGGGTGGGCGAGCCAGGGGGTGA  
 GCGGGGCCACCCCTGCCAGCTCAGGATTTGGCGGGCGATGTACCCCTCAGGGATTGGCG  
 GCGGAAGTCCCGCCCTGCGCGGCTGAGGGGCGCCCTGAGGGCCAGCACTGGCGTCT

**FIGURE 23**

MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLLEPAQRRARLEGL  
 RYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSAETYSRMRLKLVN  
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELALETP  
 MEAAELDEQREKLVLSAECQLVTTVAVVPGLELVTTQNVYFYDGSTERVETEEGIGYDFRRP  
 LAQLREVHLRRFNLRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQPGPIPPHTQV  
 RNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRTYNDL  
 SQYPVFPWVLQDYVSPTLDLSNPAVERDLSKPIGVVNPKHAQLVREKYESFEDPAGTIDKFH  
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAAWQARLESFADVKELIP  
 EFFYFPDFLENQNGFDLGCQLTNEKVGDDVLPWASSPEDFIQQHRQALESEYVSAHLHEW  
 IDLIFGYKQRGPAAEEALNVFYCYEGAVDLDHVTDERERKALEGIISNFGQTPCQLLKEP  
 HPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF  
 SFSKDPTMGSHKTQRLLSGPWVPGSGVSGQALAVAPDGKLLFSGGHWGSLRVLTALPRGKLL  
 SQLSCHLDVVTCLALDTCGIYLISGSRDTCMVWRLHQQGLSVGLAPKPVQVLYGHGAAVS  
 CVAISTELDMAVSGSEDGTVIIHTVRRGQFVAALRPLGATFPGPFIHFLALGSEQIVVQSSA  
 WERPGAQVTVSLHLYSVNGKLRLASPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA  
 PPLPMKVAIRSVAVTKERSHVLVGLEDGKLIVVAGQPSEVRSSQFARKLWRSSRRISQVSS  
 GETEYNPTEAR

**N-glycosylation site.**

amino acids 677-681

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 985-989

**Tyrosine kinase phosphorylation site.**

amino acids 56-65, 367-376, 543-551

**N-myristoylation site.**

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,  
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,  
 873-879, 912-918, 954-960

**FIGURE 24**

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC  
 CACGGCCACCTTGTGAACTCCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT  
 CCAAAGGCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCTGGGGCTCTTC  
 TGGACCCCTTAAGTGGGTACTGGCCCTGGGCCAATGCGTCTCGCTGGAGCCTTTGCCCTCCTT  
 CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCC  
 GCACACTCCGTTACCACACTGGGTCAATTGGCATTGGAGCCCTCATCCTGACCCTTGTGCAG  
 ATAGCCCGGGTCATCTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCCTGTAGC  
 CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCC  
 TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA  
 AATGCGTTCATGCTACTCATGCGAAACATTGTCAGGGTGGTGTCTCGGACAAAGTCACAGA  
 CCTGCTGCTGTTCTTTGGGAAGCTGCTGGTGGTCGGAGGCGTGGGGGTCTGTCTTCTTTT  
 TTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC  
 TGGCTGCCCATCATGACCTCCATCCTGGGGGCTATGTCATCGCCAGCGGCTTCTTCAGCGT  
 TTTCCGCATGTGTGTGGACACGCTCTTCTCTGCTTCTTGGGAAGACCTGGAGCGGAACAACG  
 GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC  
 GAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGAAGCAGCTCCGGCCCTGATCCAGGACTGC  
 ACCCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT  
 AAAAAAAGGTTTTAGGCCAGGCGCCGTGGCTCACGCCTGTAATCCAACACTTTGAGAGGCTG  
 AGGCGGGCGGATCACCTGAGTCAGGAGTTTCGAGACCAGCCTGGCCAACATGGTGAAACCTCC  
 GTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCTATCCAGCTAC  
 TCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTGCACTGAGCCGAGA  
 TCGCGCCACTGCATCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAA  
 AAAGATTTTATTAAAGATATTTTGTTAACTC



**FIGURE 25**

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGLF  
WTLNWLALGQCVLAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ  
IARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK  
NAFMLLMRNIVRVVLDKVTDLLFFGKLLVVGGVGVLSFFFFSGRIPGLGKDFKSPHLNYY  
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYYSKSLKILGKKK  
EAPPDNKKRKK

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**FIGURE 26**

GAGTCTTGACCGCCGCCGGGCTCTTGTTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGT  
 GGCT**ATG**TTTCGTGTCCGATTTCCTCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC  
 TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTT  
 CAGTGTGACCACGTGCAATATACGCTGGTTCAGTTTCTGGGTGGCAAGAATTGAACTGC  
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAACTGTGGAGCTAATGTAG  
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGG  
 CCAGTCAATGTCGTCAATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA  
 TGACCTTGAAGTTCCCGCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT  
 CAGGAAATGACAGTGATGGGTGAGAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA  
 GTGGAGCAAACCATGCGGAGGAGGCAGCGCGAGAGTGGGAGGCCCGGAGAAGAGACATCCT  
 CTTTGA CTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG  
 CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGCCCATCGTTGGACTAACAGAC  
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTTCGACGG  
 CCACGTTTCCCGCCACAACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA  
 CACGGATCTCCTTTGAGTATGACCTCCGCCTGGTGCTCTACCAGCACTGGTCCCTCCATGAC  
 AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA  
 GCGGCTCCAGGAGTTCCCTTG CAGACATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTCC  
 AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAATGATTGAAGAGTCTGCAAATAAA  
 TTTGGGATGAAGGACATGCGCGTGCAGACTTTCAGCATTCATTTTGGGTTCAAGCACAAAGTT  
 TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT  
 CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG  
 TACCATGGCCTGGAACTCGCCAAGAAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTGC  
 CTTTGCACCAACCTCGTCATCTCCCAGGGGCCCTTCTCTGTACTGCTCTCTCATGGAGGCAC  
 TCCAGATGTGATGCTGTTCTCTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA  
 AGTCCTTTGTGTGTTTCGACAAAGAACCGCGCTGCAAACCTGCTGCCCTGGTGATGGCTGCC  
 CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC  
 GGACAGGAAGAACTTTTTTGGGAGGGCGTTTGAGAAGGCAGCGGAAAGCACCAGCTCCCGGA  
 TGCTGCACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT  
 CTGGACGCACTTATTTCCCTCCTGTCT**TAG**GAAATTTGATTCTTCCAGAATGACCTTCTTATT  
 TATGTAACCTGGCTTCATTTAGATTGTAAGTTATGGACATGATTTGAGATGTAGAAGCCATT  
 TTTTATTAATAAAATGCTTATTTTAGGAAA

**FIGURE 27**

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF  
LEHKEQFHYFILINCGANVDLLDILQPEDTIFVCDSHRPVNVVNVYNDTQIKLLIKQDDD  
LEVPAYEDI FRDEEEDEEHSGNDSGSEPSEKTRLEEEIVEQTMRRRQRREWEARRRDILF  
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAI VGLTDQWVQDKITQMKYVTDVGLQRH  
VSRHNRNEDEENTLSVDC TRISFEYDLRLVLYQHWSLHDSL CNTSYTAARFKLWSVHGQKR  
LQEF LADMGLPLKQVKQKFQAMD ISLKENLREMI EESANKFGMKDMRVQTF SIHFGFKHKFL  
ASDVVFATMSLMESPEKDGSGTDHFTI QALDSLRSNLDKLYHGLELAKKQLRATQQT IASCL  
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKSFVCSTKNRRCKLLPLVMAAP  
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNNHFDLSVIELKAEDRSKFL  
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GTACCTCAGCGAGCGCCAGGCGTCCGGCCGCCGTGGCTATGNTCGTGTCCGATTTCCGCA  
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCTCGGANGTGGAT  
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT  
GGTTCAGATTCTGGGTGGCAAGAACTTGAACATGCATTTCTTGAGCATAAAGAACAGTTTC  
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT  
GAAGACACTATATTCTTTGTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA  
CGATACCC

**FIGURE 29**

CAGGAACCCCTCTCTTTGGGTCTGGATGTTGGGACCCCTTTCCAGTACCATTATTTTCTAGTGAAC  
 CACGAAGGGAGCATACCAGAAAAACACCCCTCAACCCAAAGGAATAGACTACAGCCCCAATTG  
 GCTGACTTTTGGCTATAGAAAAAGAAAGGAACGAAAGAGACAGTTTATTTTGGAAAGCTAA  
 GTCTTCCCTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTTACAGCTTTTAACAATT  
 GAGTAAAGTACGCTCCGGTCACCATGGGTGACAGCCGCCCTGGGTCCCGTCTGGGCAGCGCTC  
 CTGCTCTTTTCTCCTGATGTGTGAGATCCGTATGGTGGAGCTCACCTTTGACAGAGCTGTGGC  
 CAGCGGCTGCCAACGGTGCTGTGACTCTGAGGACCCCTGGATCCTGCCCATGTATCCTCAG  
 CCTCTTCTCCGGCCGCCACGCCCTGCCTGAGATCAGACCCCTACATTAATATACCATC  
 CTGAAGGGTGACAAAGGGGAGCCAGGCCCAATGGGCCCTGCCAGGGTACATGGGCAGGGAGGG  
 TCCCCAAGGGGAGCCTGGCCCTCAGGGCAGCAAGGGTGACAAGGGGGAGATGGGCAGCCCCG  
 GCGCCCGTGCCAGAAGCGCTTCTTGCCCTTCTCAGTGGGCCGCAAGACGGCCCTGCACAGC  
 GGCAGGACTTCCAGACGCTGCTCTTCCGAAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGA  
 CATGGGCACCGCCAGTTTGTGCTCCCTGCGTGGCATCTACTTCTTCAGCCTCAATGTGC  
 ACAGCTGGAATTACAAGGAGAGCTACGTGCACATTATGCATACCCAGAAAGAGGCTGTGCATC  
 CTGTACGCGCAGCCAGCGAGCCAGCATCATGACAGCCAGAGTGTGTATGCTGGACCTGGC  
 CTACGGGGACCGCTCTGGGTGCGGCTCTTCAAGCGCCAGCGCGAGAACGCCATCTACAGCA  
 ACGACTTTCGACACCTTACATCACCTTTCAGCGGCCACCTCATCAAGCCGAGGAGCAGCATAGG  
 CCTCTGGGCGACCCCTCCCGGTGGAGAGCTCAGGTGCTGGTCCCGTCCCTTGAGGGCTCAG  
 TTTGCACTGCTGTGAAGCAGGAAGGCCAGGGAGGTCCCGGGGACCTGGCATTTCTGGGGAG  
 CCCTGCTTCTATCTTGGCTGCCATCATCCCTCCAGCCTATTTCTGCTCCTCTTCTCTCT  
 TGGACCTATTTTAAAGAGCTTGCTAACCTAAATATTCTAGAACCTTTCCAGCCTCGTAGCCC  
 AGCACTTCTCAAACCTTGGAAATGCATGCGAATCACCCGGGTTTCGTGTAAATGCAGATTCT  
 GACTCAGCAGGTCTGAGTGGGTCCAGGATTCTGTGTTTCTCATATGTTCTGGGTGATGCTG  
 ATGGGGTCAGTCTATGAACCACTGGAGCAACAGGTTCTAGGACTTTCTCAATATTCTAG  
 TACTTTCTGAACATTCTGGAATCCTCCCCACATTCTAGAATTCTCCCAACATTTTTTTTTCT  
 TGAGACAGAGTCTTGTCTCTGTGCCCAGGCTAGAGTGCAGTGGTGCAATCTCAGTTCACTGC  
 AACCTCTGCTCCTCCCGGTTCAGCGATTCTTCTGCTCAGCCTCCCTAGTGGCTGGGATTAC  
 AGGCGCCTGCTACCATGCCCTGCTAATTTTTTGTATTTTAGTAGAGATGGGGTTTCAACATA  
 TTGGCCAGGCTGGTCTTGAACCTCTGACTTCAGGTGACCCAGCCGCTCGGCCCTCTCAAAAT  
 GCTGGGATTACAGGTGTGAGCCACCGTGCCTGGCCAATTTCAACATTTCTAAATTTCTCTCAT  
 CCTCCAGGGCTCCCGGTGCTATGTTCTCTTTACCCCTTCCCCCTCTTCTCTGCTCAGGCC  
 TGCACCACTGCAGCCACCGTTTCATTATTTCATTAAACACTGAGCACTCACTCTGTGCT  
 GGGTCCCGGGAAGGGTGAGGGGGTCAACACAGGCCCTGCCCTGCCCTCAGTGAATGGCCA  
 GTCCAGCCCAGGCGGGGAGAGATGTGTACATAGGTTTTAAAGCAGACCCAGAGCTCATGGGG  
 GCCTGTGTTCTGGGTGTTCAAGGTGCTGCTGGTCTCCTCCATTACCCACTGCTCCCCAAGGCTGG  
 TGGGACGGGTCCCGGTGGCAGGGGAGGTATCTCCTTCCCGTTCCTCATCCACTGCCGCA  
 TGCTACCTGTTACAGCAAAACCCAGGGGGCTTGGCCAGGTCAAGGGTCTGTGAGGAGAGG  
 ACCCAGGAGTGTGGGGGCTTGTGGGGGTGAAGTGGCCCCGAGGAATGGAACCCACACCCA  
 TAGCTTCCCCACAGCTGATACGGCATCTGCGAGAAAGACTGCCCCCTCTCACTGGGATCCC  
 CTTCCTGCCCTCCTCCAGGGCTCTGCCAGGGCTTGCTCAGTCCCTTCCACCAAAGTCACTCT  
 GAACCTCCGTTTCCCCAGGGCCCTCAGCTGCCCTCAGACACTGATGTCTGTCTCCAGGTGCT  
 CTCTGCCCTCATGCCCCCTTCACCGGCCAGTGCCCGCATCTCCAGGCTTTATCAAGGTG  
 CTAAGCCCGGGGTGGCGAGCTTCCTCGTCTCAGAGCCCTCCTCCGGCTTGGTGTGCTTTCAT  
 AAACACCTGAGGAGAAGGGCCACGGAAGCCCAAGGCTTTAGAGCCCTCAGCAGGCTCTGGGG  
 AGCTAGAGCAAGGAGGGACCTCAGGCCCTCCGTTTCTTCTCCAGGGTGGGTGGCTGGTGGT  
 GTTCCCTAGCTTTCCAAACCCAGGTGGCCTGCCCTTCTCCCAAGGGAGGGCGCCCTCCG  
 CCATTGGTGCTCATGCAGACTCTGGGGCTGAGGTGCCCGGGGGGTGATCTGGTGTGCAC  
 AGCCGAGGAGCCGTGGCTTCCATGGCCAGATGACGGAACAGGGTCTGACCAAGTCCAGGA  
 AGACTGTGCTATAAACACCCCTGCCTGATCCTGCCCTGCCCTGACCCGCCACGCCCTGCC  
 GTCCAGCATGATTAAAGATGCTGTCTCCTTGGAAAAA

## **FIGURE 30**

MVTAALGPVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSGRPH  
ALPEIRPYINITILKGDKGDPGMPGLPGYMGREGPGPGQGSKGDKGEMGSPGAPCQKRF  
FAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET  
YVHIMHNQKEAVILYAQPSESRIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYIT  
FSGHLIKAEDD

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **N-glycosylation site.**

amino acids 72-75

#### **Clq domain proteins.**

amino acids 144-178, 78-111 and 84-117

**FIGURE 31**

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGACTG  
 AGGCCGCGGGCTGCCCGCCCGGCTCCCTGCGCCGCCGCCCTCCCGGGACAGAAGATG  
 CTCCAGGGTCCCTCTGCTGCTGCCGTGCTCCTGCTACTGGCCCTGGGGCTCGGGGTGACGG  
 GCTGCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCATGCCCGCCAGGGG  
 ACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCAT  
 CACCATGCTCGACGCAGGCAGCTTTGCCGGCTGCCGGGCTGCAGCTCCTGGACCTGTCAC  
 AGAACAGATCGCCAGCCTGCCAGCGGGTCTTCCAGCCACTCGCCAACCTCAGCAACCTG  
 GACCTGACGGCCAACAGGCTGCATGAAATACCAATGAGACCTTCCGTGGCCTGCGGGCCCT  
 CGAGCGCTCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCCCTCGACACGC  
 TCGACCGCTCCTGGAGCTCAAGCTGCAGGACAACGAGCTGCGGGCACTGCCCCGCTGCGC  
 CTGCCCCGCTGCTGCTGCTGCTGAGCCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGCAT  
 CCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGTCTGGGGCTGCAGCAGCTGGACG  
 AGGGGCTCTTCAGCCGCTTCGCGCAACCTCCACGACCTGGATGTGTCCGACAACAGCTGGAG  
 CGAGTGCCACTGTGATCCGAGGCCCTCCGGGGCTGACCGCTCGCGTGGCCGGCAACAC  
 CCGCATTTGCCAGCTGCGGGCCAGGACCTGCGGGCTGGTGCCCTGCAGGAGCTGGATG  
 TGAGCAACCTAAGCCTGCAGGCCCTGCTGCGGACCTCTCGGGCTCTTCCCCGCTGCGG  
 CTGCTGGCAGCTGCCCCGAACCCCTTCAACTGCGTGTCGCCCTGAGCTGGTTTGGCCCTG  
 GGTGCGCGAGAGCCACGTCAACTGGCCAGCCTGAGGAGACGCGCTGCCACTTCCCGCCCA  
 AGAACGCTGCGCGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCAGCCACCACC  
 ACCACAGCCACAGTGCCACACACGAGGCCCTGGTGCGGGAGCCCAAGCCTGTCTCTTAG  
 CTGGCTCCTTACCTGGCTTAGCCCCACAGCGCCGCCACTGAGGCCCCAGCCCGCCCTCA  
 CTGCCCCACCGACTGTAGGGCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTC  
 AATGGGGGCACATGCCACCTGGGGACACGGCACCTGGCGTGCTTGTGCCCGAAGGCTT  
 CACGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGACACGGCCAGCCCTACACCAAGTCA  
 CGCCGAGGCCACACGGTCCCTGACCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGC  
 GTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTA  
 TCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTG  
 AGTACACGGTCACCCAGCTGCGGCCCAACGCCACTTACTCCGTCTGTGTATGCCTTTGGGG  
 CCGGGCGGGTGCCGGAGGGCGAGGAGGCCCTGCGGGGAGGCCCATACCCCCAGCCGTCCA  
 CTCCAACACGCCCCAGTCAACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCG  
 CCTGGCCGCGGTGCTCCTGGCCGCGCTGGCTGCGGTGGGGGAGCCCTACTGTGTGCGCGG  
 GGGCGGGCCATGGCAGCAGCGGCTCAGGACAAGGGCAGGTGGGGCAGGGGTGGGGCCCT  
 GGAACCTGGAGGGAGTGAAGGTCCCTTTGGAGCCAGGCCGAAGGCAACAGAGGGCGGTGGAG  
 AGGCCCTGCCAGCGGTCTGAGTGTGAGGTGCCACTATGGCTTCCAGGGCCTGCGCTC  
 CAGTCAACCCCTCCACGCAAAGCCCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCG  
 GGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCAGTAAGTTCTCAGTCC  
 CAACCTCGGGATGTGTGCAGACAGGGCTGTGTACCACAGCTGGGCCCTGTTCCCTCTGGA  
 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTACAGTCCCCAGAAC  
 CGAGTGCTATGAGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCG  
 GGCCTGCCATGTGCTGGTAACGCATGCCTGGGTCTGCTGGGCTCTCCCACTCCAGGCGGA  
 CCTGGGGGCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTG  
 TGACTCTAGTCTTGGCCCCAGGAAGGAAGGAACAAAGAAACTGGAAGGAAGATGCTTTA  
 GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCCATTTATTCTG  
 GAAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTGTAAAGACAACGATGATATG  
 AAGGCCTTTTGTAAGAAAAATAAAGATGAAGTGTGAAA

**FIGURE 32**

MCSRVP LLLPL LLLLLALGPGVQGCPSGCQCSQPQT V FCTARQGT TVPRDVPPDTVGLYVFEN  
GITMLDAGS FAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR  
RLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRL LLLDL SHNSLLALEP  
GILDTANVEALRLAGLGLQLDEGLFSRLRNLDLDVSDNQLERVP PVIRGLRGLTRLRLAG  
NTRIAQLRPEDLAGLAALQELDVS NLSLQALPGDLSGLFPRLRLAAARNPFNCVCPLSWFG  
PWVRESHVTLASPEETRCHFP PKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALS  
SSLAPTWLSPTAPATEAPSPSTAPPTVGPVPQPQDCFPSTCLNGGTCHLGTRHHLACLCE  
GFTGLYCESQMGQGTRPSPTPTVTPRPPRSLTLGIEPVSPSTSLRVGLQRYLQGSSVQLRSLRL  
TYRNLSGPDKRLVTLRLPASLA EYTVTQLRPNATYSVCMPLGPRVPEGEEACGEAHTPPA  
VHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRGRAMAAAAQDKGQVGPAG  
PLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI



**FIGURE 33**

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCAT  
 CTTTCATCATTCATATGAGGAAATAAGTGGTAAAATCCTTGGAAATACA**ATG**AGACTCATCAG  
 AAACATTTACATATTTTGTAGTATTTGTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAG  
 AAGAAAGGGAAGCTGATGACCAACTGCTCCAACATGTCTCTAAGAAAGGTTCCCGCAGACTTG  
 ACCCAGCCCAACGACATCGGATTTATCCTATAACCTCCTTTTCAACTCCAGAGTTTCAGA  
 TTTTCATTCTGTCTCCAACTGAGAGTTTTGATTCTATGCCATAACAGAATTCACACAGCTGG  
 ATCTCAAAACCTTTGAATTCACAAGGAGTTAAGATATTTAGATTTGTCTAATAACAGACTG  
 AAGAGTGTAACCTTGGTATTTTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTTAATGACTT  
 TGACACCATGCCTATCTGTGAGGAAGCTGGCAACATGTACACCTGGAATCCTAGGTTTGA  
 GTGGGGCAAAAATACAAAATCAGATTTCCAGAAAATTGCTCATCTGCATCTAAATACGTCTC  
 TTCTTAGGATTCAGAACTCTTCTCATTATGAAGAAGGTAGCCTGCCATCTTAAACACAAC  
 AAAACTGCACATTGTTTTACCAATGGACACAATTTCTGGGTTCTTTGCGTGATGGAATCA  
 AGACTTCAAAAATATAGAATGACAATATAGATGGCAAAAGCCAATTTGTAAGTTATGAA  
 ATGCACGAAATCTTAGTTTAGAAAATGCTAAGACATCGGTTCTATGTGCTTAATAAGTTGA  
 TTTACTCTGGGACGACCTTTTCCTTATCTTACAAATTTGTCATATACATCAGTGGAACT  
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAAATTCATTTGACTAC  
 TCAAAATACGTAAATGAGAATATAAAAATGGAGCATGTACATTTTCAGATGCTTTTACATTC  
 ACAGGATAAAATCTATTTGCTTTTGACCAAAATGGACATAGAAAACCTGACAAATATCAAATG  
 CACAAATGCCACATGCTTTTCCGAATTTATCCTACGAAATTCAAATTTAAATTTTGTGCC  
 AATAATATCTTAACAGACGAGTTGTTTAAAAGAAGTCTCAACTGCCTCACTTGAACAACTCT  
 CATTTTGAATGGCAATAAACTGGAGACACTTTCTTTAGTAGTTGCTTTGCTAAACACACAC  
 CTTTGGAACTTTGGATCTGAGTCAAATCTATTACAACATAAAAAATGATGAAAATTTGCTCA  
 TGGCCAGAACTGTGGTCAATATGAATCTGTCATACAATAAATTTGCTGATTCGTCTTCAG  
 TGCTTTGCCCAAAGTATTCAAATACCTTGACCTAAATAAATACCAAAATCCAACTGACCTA  
 AAGAGACTATTTCACTGATGGCCTTACGAGAACTAAATATGCAATTTAAATTTCTTAATCTGAT  
 CTCCCTGGATGCAGTCATTTTCAGTAGACTTTCAGTTCTGAACATTTGAAATGAACATCTTCT  
 CAGCCCATCTCTGGATTTTGTTCAGAGCTGCCAGGAAGTTAAAACCTCTAAATGCGGGAGGAA  
 ATCCATTCGGGTGACCTGTGAAATTAATAAATTTTTCAGTCTGAAACATATTCAGAGGTC  
 ATGATGGTTGGATGGTCAGATTATACACCTGTGTAATACCCTTTAAACCTAAGGGGAACTAG  
 GTTAAAAGACGTTTCATCTCCACGAATTTATCTTGCAACACAGCTCGCTTTGATTGTCACCAATG  
 TGGTTATTATGCTAGTTCTGGGGTTGGCTGTGGCCTTCTGCTGTCTCCACTTTGATCTGCC  
 TGGTATCTCAGGATGCTAGGTCATATGCACACAAACATGGCACAGGGTTAGGAAAAACACCCA  
 AGAACAACCTCAAGAGAAATGTCCGATTCACGCAATTTATTTCATACAGTGAACATGATTTCTC  
 TGTGGGTGAAGAAATGAATGTATCCCAATCTAGAGAAGGAAGATGGTTCTATCTTGATTTGC  
 CTTTATGAAAGCTACTTTTGACCTGGCAAAAGCATTAGTGAAAATATTTGTAAGCTTCATTTGA  
 GAAAAGCTATAAGTCCATCTTTGTTTTGTCTCCAACTTTTGTCCAGAATGAGTGGTGCCATT  
 ATGAATTTCACTTTGGCCACCAACATCTTCCATGAAAATTTCTGATCATATAAATTTCTATC  
 TTACTGGAACCCATTCATTTCTATTGCAATTCACACAGGTATCATAACTGAAAGCTCTCCCT  
 GGAAAAAAGACATACTTGAATGGCCAAAGGATAGGCGTAAATGTGGGCTTTTCTGGGCCAA  
 ACCTCTCAGCTGCTATTAATGTTAATGTATTAGCCACCAGAGAAATGTATGAATCGCAGACA  
 TTCACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCTCTGATGAGACAGATTGCT  
**ATAA**AAATCCCAAGTCTTGGGAGTTGGGGACCCATACACTGTTGGGATGTACATTTGATA  
 CAACCTTTATGATGGCAATTTGACAAATATTTATTAATAAATAAATTTGGTTATTTCCCTTCATA  
 TCGATTTCTAGAAGGATTTTCAAGAATGTATCCTATAGAAACACCTTCACAGAGTTTATAAGG  
 GCTTATGGAATAAAGGTGTTCAATCCAGGATTTGTTTATAATCATGAAAATGTGGCCAGGTGCA  
 AGTGGCTCACTCTTGTAATCCAGCACTATGGGAGGCCAAGGTGGCTGACCCAGGCTTCAAG  
 GAGATGGAGACCATCTGGCCAACTAGGTGAAACCTGTCTCTACTAAATAATACAAAATTA  
 GCTGGGCGTATGGTGCAGCCTGTAGTCCAGCTACTTGGGAGCTGAGGCAGGAGAAATCG  
 CTTGAACCCGGGAGGTGGCAGTTGCAGTGAGCTGAGATCGAGCCACTGCCTCCAGCCTGGT  
 GACAGAGCGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAAGAAAAATGGAAAAACATCC  
 TCATGGCCACAAAATAAGGCTCAATTTCAATAAATATAGTACATTAATGTAATATAATATTA  
 CATGCCACTAAAAAGAATAAGGTAGCTGTATATTTCCTGGTATGAAAAAACATATAATAT  
 GTTATAAACTATTAGGTTGGTGCAAACTAATTTGGTTTGTGCTTTGCAATTTGAATGGCATGAA  
 ATAAAAGTGTAAAGAACTATACACAGATAGTAACAGTGGTTTGGGCTGGGAGGTTGGA  
 TTAACGGGAGCATTTGATTTCTATGTTGTTGTTATTTCTATAATGTTTGAATGTTTGAATGA  
 ATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

**FIGURE 34**

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQ  
LQSSDFHVS SKLRVLILCHNRIQQDLKTFEFNKE LRYLDLSNNRLKSVTWYLLAGLRYLDL  
SFNDFDTMPICEEAGNM SHLEILGLSGAKIQKSD FQKIAHLHLNTVFLGFRTLPHYEEGSLP  
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL  
LNKVDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR  
VFYIQQDKIYLLLT KMDIENLTISNAQMPHMLFPNYPTK FQYLN FANNILTDELFKRTIQLP  
HLKTLILNGNKLETSLVSCFANNTPLEHLDLSQNL LQHKNDENC SWPETVVNMNLSYNKLS  
DSVFRCLPKSIQILD LNNNQIQTVPKETIHLMALRELNIAFNFLTDLPGCSHFSRLSVLNIE  
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLE TYSEVMMVGWSDSYTCEYPLN  
LRGTRLKDVHLHELSCNTALLIVTIVVIMLVGLAVAFCC LHFDPWYLRMLGQCTQTWHRV  
RKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI  
VSFIEKSYKSIFVLSPNFVQNEWCHYEFYFAHHNLFHENS DHIIILILLEPIPFYCIPTRYHK  
LKALLEKKAYLEWPKDRRKCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM  
RTDCL

**FIGURE 35**

GGGGGCTTTCTTGGGCTTGCTGCTTGGAAACACCTGCCTCCAAGGACCGGCCTCGGAGGGGTGCGCGGAAAGG  
 GAGGGAGAGGAAGGGGGGGGGCCGGCCCCCTGCGCCGCGCCCGCGCCTCTGCGCGCCCTGTCCGCCCGGGC  
 CCAGCCCGCCCGCCCGGGCTCGAGCGCCAGCCAGCGCGCCCTTCCCGCGCCCGCCAGCGCGCCCTCT  
 CTGCTGTGCCCTGCGCCCTTGCCCCGCGCCAGCTTCTGCGCCCGCAGCCCGCCCGCGCCCGCGGTGACCGTGA  
 CCTGCCCTGGGCGCGGGGCGGAGCAGGCATGCTCCCCCGGGGACCGCTACCCAGCGCTGGCCCTGGTGCTC  
 CTGGCAGTGACCTGGCCGGGGTGGAGCCCGAGGCGCAGCCCTCGAGGACCTGATTATTACGGGCGAGGAGAT  
 CTGGAGCCGGGAGCCCTACTACGCGCGCCCGGAGCCCGAGCTCGAGACCTTCTCTCCGCCGCTGCTGCGGGGC  
 CCGGGGAGGAGTGGGAGCGCGCCCGCAGGAGCCCGAGCCGCCCAAGAGGGCCACCAAGCCCAAGAAAGCTCCC  
 AAGAGGGAGAAGTCCGCTCCGGAGCCGCTCCACCAGGTAAACACAGCAACAAAAAGTTATGAGAACCAAGAG  
 CTCTGAGAAGGCTGCCAACGATGATCAGTGTCCGTGTGGCCGTGAAGATGTCAGAGAGAGTTGCCACCTC  
 TTGGTCTGGAACCTTAAAAATCACAGACTTCCAGCTCCATGCCTCCACGGTGAAGCGCTATGGCTGGGGGA  
 CATCGAGGGAGACTCAACATCCAGGCGGGCATTAAATGAAATGATTTTATGACGGAGCGTGGTGCGCGGGAAG  
 AAATGACCTCCAGCAGTGGATTGAATGGATGCTCGGCGCTGACCAGATTCACTGGTGTCTATCACTCAAGGA  
 GAACTCCCTCTGGCTGAGTGACTGGGTGACATCTATAAGTTCATGGTGAGCAATGACAGCCACAGTGGGTG  
 ACTGTTAAGAATGGATCTGGAGCATGATATTTGAGGGAACACTGAGAGAGGAGATCCCTGTCTCAATGAGCT  
 ACCCGTCCCCATGGTGGCCCGCTACATCCGCATAAACCTCAGTCTGGTTTGATAATGGGAGCATCTGCATGA  
 GAATGAGAGTCTGGGCTGCCACTGCCAGATCTTAATAATTATTATCACCGCCGGAACGAGATGACCACCACT  
 GATGACTGGATTTTAAGCACCAATATTAAAGAAATGCGCAGTTGATGAAAGTTGTGATGAATGTGTCC  
 CAATATCACCAGAAATTACAACATTGGAAAAAGCCACGAGGCCCTGAAGTGTATGCTGTGAGATCTCAGATC  
 ACCCTGGGAGCATGAAGTCGGTGAGCCCGAGTTCCACTACATCGCGGGGCCACGCGCAATGAGGTGCTGGGC  
 CGGGAGCTGCTGCTGCTGCTGGTGCATTTGCTGTGTCAGGAGTACTTGGCCCGGAATGCGCGCATCGTCCACT  
 GGTGGAGGAGACGCGGATTCACGTCTCCCTCCCTCAACCCCGATGGCTACGAGAAGGCCCTACGAGGGGCT  
 CGGAGCTGGGAGCTGGTCCCTGGGACGCTGGACCCAGCATGGAATTGACATCAACAAACAACTTTCCCTGATT  
 AACACCGCTGCTCTGGGAGGCGAGGATCGACAGAATGTCCCAGGAAAGTTCCCAATCACTATATTGCAATCCC  
 TGAGTGGTTTCTGTGCGAAAAATGCCAGGTGGCTGCCGAGACGAGCAGTCAAGCTGGATGGAAAAAATCCC  
 CTTTGTGCTGGCGGCCAACCCTGACGGGCGGCGAGCTGGTGGTGGCGTATCCCTACGACCTGGTGGCGTCCCC  
 TGGAAACGCGAGGAACACACCCCCACCCCGATGACCAAGTGTCCGCTGAGGAGTGGCTCTCTATGCTCCAC  
 ACACCGCTCATGACAGACGCCCGGAGGAGGCTGTGCCACACGAGGAGCTTCCAGAAGGAGGAGGCGACTGTCA  
 ATGGGCGCTCCTGGCACACCTGCTGCGTGGAGTCTGAACGATTTTCAGCTACCTTCATACAACTGCTTCGAAGT  
 TCCATCTACGTGGCTGTGATAAATACCCACATGAGAGCCAGCTGCCCGAGGATGGGGAATAACCGGGAATC  
 TCTGATCGTGTTCATGGAGCAGGTTTCATCTGGCATTAAAGGCTTGGTGAGAGATTTCATGGAAGAAAGGAATCC  
 CAAACGCCATTATCTCCGTAGAAGGCATTAAACCATGACATCCGAACAGCCAACGATGGGGATTACTGGCGCCTC  
 CTGAACCTTGGAGAGTATGTGCTCAGCAAAAGGCCGAAGTTTCACTGATCCACCAAGAATGTATGGTTGG  
 TATGACATGGGGGCCCAAGGTTGTGACTTCACTTAGCAAAACAACTGCGCAGGATCCGAGAGATCATGG  
 AGAAGTTTGGGAAGCAGCCCTGACGCTGCCAGCCAGGCGGCTGAAGCTGCGGGGCGGGAAGAGACGACGCGT  
 GGGTGAACCTCTCGGGCCCTTGAGACTCGCTGGGACCCATGCAAAATTAACCAACCTGGTAGTAGCTCCATAG  
 TGGACTACTCACTGTTGTTTCTCTGTAATTCAAGAAGTGCTTGGAGAGAGGGTGCATTGTGAGGCGAGGTCC  
 CAAAAGGGGAGGCTGGAGGCTGAGGCTGTTTCTTTCTTTGTTTCCCAATTATCCAAATAACTTGGACAGAGCA  
 CGACAGAAAAGCTGATGGGAGTGAGGAAGTCAAGCAAGCCAACCTGGGAATCAGAGAGAGGAGGAGGAGG  
 GAGCCTGTCCGTTCAGAGCCTCTGGCTGCATGAAAAGGATTCTGGTGCTTCCCTGTTTGGCTGGCAGCAAGG  
 GTTCCACGTGCATTTCGAATTTGCACAGCTAAATTCAGCATTTCCCGAGTGGCTGCGCAACTGTGTACCA  
 TTTGAGATGCTCCAGGCGTCTTAAGAGAATCCACCTCTCTGGCCCTGGGACATTGCAAGCTGCTACAAATAA  
 ATTTCTGTGTTCTTTGACAATAGCGTCATTGCCAAGTGCACATCAGTAGGCCCTTGTGAATCTGTTTAGTCTCCT  
 TTTTCAACAAAGGAGTGTGTTTCAGAAAAGGAGAGAGGCTGAGATTCATTCCAGGATTTGTGGGCGCAAGCA  
 TGGAGCTTCTTGCACAAATTTGGGTCCATAAACAACCCCCAAAGTCCCTGCTGATCCAGTAGGCCCTGGAGGTT  
 CCCCAGGTAGGAGAGCCAGAGGTGCCAGCCTTCTTGAAGGGCCAGAAAAATTAGCCTGGATCTCCTCTTTTAC  
 CTGCTAGGACTGGAAGAGCCAGAAGTGGGGTGGCTTGAAGCCCTCTCTCTGCTTGAAGTATTGCCCTGTGTG  
 GAATTGAGTGTCTATGGGTTGGCCTCATATCAGCCTGGGAGTTATTTTGTATGTAGAATGCCAGATCTTCCA  
 GATTAGGCTAAATGTAAAGAAACCTCTAGGATTATCTGTGGAGCATGATTGGGAAGAATTTAGAAATTA  
 CTTGCAAGAAAAAGTATGTCCTACTTTTGTTAATGTTGCTGCCTCATTGACCTGGGAAAAATGAAAAA  
 AATAAAGCAAAATGGTAAGACCTTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG

**FIGURE 36**

MSRPGTATPALALVLLAVTLAGVGAQGAALEDPDYYGQEIWSREPPYYARPEPELETFSPLP  
AGPGEWERRPQEP RP PKRATKPKKAPKREKSAPEPPPGKHSNKKVMRTKSSEKAANDHS  
VRVAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGLNIQAGINENDFYDGAWCA  
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSTWVTVKNGSGDMIF  
EGNSEKEIPVLNELPVPVMVARYIRINPQSWFDNGSICMRMEILGCPLDPNNYYHRRNEMTT  
TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF  
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNPDGYEKAYEGG  
SELGGWSLGRWTHDGDIDINNFPDLNTLLWEAEDRQNVPRKVPNHYYIAIPEWFLSENATVAA  
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAYSYST  
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHES  
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGI PNAIISVEGINHDIRTANDGDYWRLL  
NPGEYVVTAKEGFTASTKNCMVG YDMGATRCDFTL SKTNMARIREIMEKFGKQPVSLPARR  
LKLGRKR RRG

**FIGURE 37**

CTAAGAGGACAAG~~ATG~~AGGCCCGGCTCTCATTTCTCCTAGCCCTTCTGTTCTTCTTGGCCAAAGCTGCAGGGG  
 ATTTGGGGGATGTGGGACCTCCAATTCCCAGCCCCGGCTTCAGCTCTTTCCAGGTGTTGACTCCAGCTCCAGC  
 TTCAGCTCCAGCTCCAGGTCGGGCTCCAGCTCCAGCCGAGCTTAGGCAGCGAGGTTCTGTTCCCGATTGCTTT  
 TTCCAATTTACCCGGCTCCGTGGATGACCGTGGGACCTGCCAGTGCTCTGTTTCCCTGCCAGACACACCTTTC  
 CCGTGGACAGAGTGGAAAGCTTGGAAATTCACAGCTCATGTTCTTCTCAGAAGTTTGAGAAAGAACTTTCTAAA  
 GTGAGGGAATATGTCCAATTAATTAGTGTGTATGAAAAGAACTGTTAAACCTAACTGTCCGAATTGACATCAT  
 GGAGAAGGATACCATTTCTTACACTGAACTGGAGCTTCGAGCTGATCAAGGTAGAAGTGAAAGAGATGGAAAAAC  
 TGGTCATACAGCTGAAGGAGAGTTTGGTGGAGCTCAGAAATTGTTGACCAGCTGGAGGTGGAGATAAGAAAT  
 ATGACTCTCTTGGTAGAGAAGCTTGAGACACTAGACAAAAACAATGTCTTGCCATTGCCTGGAGAAATCGTGGC  
 TCTGAAGACAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAAACACCCCTCTGCTGCCACCTCTCCCACTC  
 CAGGGAGCTGTGGTCATGGTGGTGGTGAACATCAGCAACCGTCTGTGGTTCAGCTCAACTGGAGGGGTTT  
 TCTTATCTATATGGTCTTTGGGGTAGGGATTACTCTCCCGAGCATCCAACAAGAGACTGTATTGGGTGGCGCC  
 ATTGAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTACAACACACTGGATGATTTGCTATTGTATATAA  
 ATGCTCGAGAGTTGCGGATCACCTTAGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAAC  
 ATGTACAACACCGGGAATATTGCCAGAGTTAACCTGACCACCAACAGGATTGCTGTGACTCAAACCTCTCCCTAA  
 TGCTGCCATAATAACCGCTTTTATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGAATG  
 GATTGTGGGTATTTATTCAACTGAAGCCGAGCTGGTAACATGGTGATTAGTAAACTCAATGACACCACACTT  
 CAGGTGCTAAACACTTGGTATACCAAGCAGTATAAACCATCTGCTTCTAACGCCCTCATGGTATGTGGGGTTCT  
 GTATGCCACCCGTACTATGAACACCCAGAACAGAGAGATTTTTACTATTATGACACAAACACAGGGAAGAGGG  
 GCAAACAGACATTGTAATGCATAAGATGCAGGAAAAAGTGCAGAGCATTAACTATAACCCCTTTGACCAGAAA  
 CTTTATGTCTATAAGATGGTTACCTCTGAATTATGATCTTTCTGCTTGCAGAAGCCCCAG~~TAA~~GCTGTGTTA  
 GGAGTTAGGGTGAAAGAGAAAAATGTTTGTGAAAAAATAGTCTTCTCCACTTACTTAGATATCTGCAGGGGTG  
 CTAAAAGTGTGTTCATTTTGCAGCAATGTTTAGGTGCATAGTTCTACCACACTAGAGATCTAGGACATTTGTCT  
 TGATTTGGTGAGTTCTCTTGGGAATCATCTGCCTCTTCAGGCGCATTTTGCAATAAAGTCTGTCTAGGGTGGGA  
 TTTGTCAGAGGTCTAGGGGCACTGTGGGCTAGTGAAGCCTACTGTGAGGAGGCTTCACTAGAAGCCTTAAATTA  
 GGAATTAAGGAACCTTAAACTCAGTATGGCGTCTAGGGATTCTTTGTACAGGAAATATTGCCAATGACTAGTC  
 CTCATCCATGTAGCACCCTAATTTCTCCATGCTGGAAGAAACCTGGGACTTAGTTAGGTAGATTAATATCT  
 GGAGCTCCTCGAGGGACCAAACTCTCCAACCTTTTTTTCCCTCCTAGCACCTGGAATGATGCTTTGTATGTTG  
 CAGATAAGTAAATTTGGGCATGCTTATATATTCTACATCTGTAAAGTGTGAGTTTATGGAGAGAGGCCCTTTT  
 ATGCATTAATTTGTACATGGCAATAAATCCCAGAAAGGATCTGATAGGCGGAGGCTGTTTTCTTTCTCTC  
 ATTTGTCACCTTACTAAAAGTCAGTAGAATCTTCTACCTCATAACTTCTTCCAAAGGCAGCTCAGAAGATTAG  
 AACCAGACTTACTAACCAATTCCACCCCCCACCACCCCTTCTACTGCCTACTTTAAAAAATTAATAGTTTT  
 CTATGGAACCTGATCTAAGATTGAAAAATTAATTTCTCTTAATTTCAATTATGACTTTTATTATACATGACTCTA  
 AGACTATAAGAAAACTGATGGCAGTGACAAAGTGCTAGCATTTATTGTTATCTAATAAAGACCTTGGAGCATA  
 TGTGCAACTTATGAGTGTATCAGTTGTTGCATGTAATTTTTGCTTTGTTTAAAGCCTGGAACCTGTAAGAAAAAT  
 GAAAAATTAATTTTTTTTCTAGGACGAGCTATAGAAAAGCTATTGAGAGTATCTAGTTAATCAGTGCAAGTGT  
 TGGAAACCTTGCTGGTGTATGTGATGTGCTCTGTGCTTTTGAATGACTTTATCATCTAGTCTTTGTCTATTTT  
 TCCCTTGATGTTCAAGTCTAGTCTATAGGATGGCAGTTTAAATGCTTTACTCCCCCTTTTAAAAATAATGAT  
 TAAAAATGTCGTTTTGAAAAAATAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 38**

MRPGLSFL LALLFFL GQAAGDLGDVGPPIPSPGFS SFGVDSSSSFS SSSSRSGSSSSSRSLGS  
GGSVSQ LFSNFTG SVDDRGT CQCSVSLPDTTFPVD RVERLEF TAHVLSQKF EKELSKVREYV  
QLISVYEKLLNLTVRIDIMEKDTISY TELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ  
LEVEIRNM TLLVEKLE TLDKNNVLAI RREIVALKTKLKECEASKDQNTPVVHPPPTPGSCGH  
GGVVNISKPSVVQLNWRGFSYLYGAWGRDYS PQHPNKGLYWVAPLNTDGR LLEYRLYNTLD  
DLLLYINARELRITYGQSGTAVYNNNMYVNM YNTGNIARVNLT TNTIAVTQTL PNAAYNNR  
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDTTLQVLNTWYTKQYKPSASNAF  
MVCGLVLYATRTMNRTEEI FYYYDTNTGKEGKL DIVMHKMQEKVQSINYNPFDQKLYVYNDG  
YLLNYDLSVLQKPQ

**FIGURE 39**

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC  
CCTCCTCCCCTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT  
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTGCTGGGGTAGGGATTACTCTC  
CCCAGCATCCAAACAAAGGNATGTATTGGGNGGCGCCATTGAATACAGATGGGAGACTGTTG  
GAGTATTATAGACTGTACAACCCACTGGATGATTGCTATTGTATATAAATGCTCGAGAGTT  
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA  
TGTACAACACCGGNATATTGCCAGAGTTAACCTGACC

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**FIGURE 40**

TCTCGCAGATAGTAAATAATCTCGGAAAGGCGAGAAAGAAGCTGTCTCCATCTTGTCTGTAT  
 CCGCTGCTCTTGTGACGTTTGTGGAGATGGGGAGCGTCTGGGGCTGTGCTCCATGGCGAGCT  
 GGAATACCATTGTTTGTGTGGAACTGCCCGTGTTTGGCTATAGCGATGCTGTCCATGGGAAAC  
 AACTCCACTGTAACTAGATTGATCTATGCACCTTTCTTGCTTGTGGAGTATGTGTAGCTTG  
 TGTAAATGTTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCTCGGATTTTGTGAGAATG  
 AGAAAGGTGTTGTCCCTGTGAACATTTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTT  
 GGTTTGGCTATGTTCTATCTCTTCTCTCTTACTAATGATCAAAGTGAAGAGTAGCAGTGA  
 TCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCTTAAATTTGCTGCAGCAATTGCAATTA  
 TTATTGGGGCATTCTTCATTCCAGAAGGAACTTTTACAACCTGTGTGGTTTTATGTAGGCATG  
 GCAGGTGCCCTTTTGTTCATCCTCATACAACCTAGTCTTACTTATTGATTTTGCACATTTCATG  
 GAATGAATCGTGGGTGAAAAAATGGAAGAAGGGAACCTCGAGATGTTGGTATGCAGCCTTGT  
 TATCAGCTCAGACTGGAATTATCTGCTGTCTTTAGTTGCTATCGTCTGTTCTTTGTCTAC  
 TACACTCATCCAGCCAGTTGTTTCAGAAAAACAAGGCGTTTCATCAGTGTCAACATGCTCCTCTG  
 CGTTGGTGCTTCTGTAAATGTCTATAGTCCAAAAATCCAAGAATCACAAACCAGATCTGGTT  
 TGTTCACAGCTTCAGTAATTACAGCTCATACAATGTATTTGACATGGTCAGCTATGACCAAT  
 GAACCAGAAACAAATTGCAACCCAACTCTACTAAGCATAAATGGCTACAATACAACAGCAC  
 TGTCCCAAAGGAAGGCGAGTCACTCCAGTGGTGGCATGCTCAAGGAATTATAGGCAATATTC  
 TCTTTTGTGTGTTGATTTTATTCCAGCATCCGTAAGTCTCAAAACAATGTCAGGTTAATAAA  
 CTGACTCTAACAGTAGTAATCTACATTAATAGAAGATGTTGGAGCTAGAAGTGAATGATG  
 ACTGGAGGATGGGGACGATGTTACCCAGAGCTGTAGATAATGAAAGGATGGTGTCACTTACA  
 GTTATTCCTTCTTCACTTACATGCTTTTCTGGCTTCACTTTATATCATGATGACCTTACC  
 AACTGGTCCAGGTATGAACCTCTCGTGAGATGAAAAGTCAGTGGACAGCTGTCTGGGTGAA  
 AATCTCTCCAGTTGGATTGGCATCGTGCCTGTATGTTTGGACACTCGTGGCACCACTTGTTC  
 TTACAAATCGTGATTTTGAAGTGAAGTCTAGCATGAAAGTCCCACTTTGATTATTGC  
 TTATTTGAAAACAGTATTCCCAACTTTTGTAAAGTTGTGTATGTTTTGCTTCCCATGTAAC  
 TTCTCCAGTGTTCGGCATGAATTAGATTTTACTGCTTGTCAATTTTGTATTCTTTACCAA  
 GTGCATTGATATGTGAAGTAGAATGAATTGCAGAGGAAAGTTTATGAATATGGTGTAGT  
 TAGTAAAAGTGGCATTATTTGGGCTTATCTCTGCTCTATAGTTGTGAAATGAAGAGTAAAA  
 ACAAATTTGTTGACTATTTTAAATATATTAGACCTTAAGCTGTTTTAGCAAGCATTA  
 GCAATGTATGGCTGCCTTTTGAATATTTGATGTGTGCTGGCAGGATACCTGCAAGAAC  
 ATGGTTTATTTTAAATTTTAAACAAGTCACTTAAATGCCAGTTGCTGAAAAATCTTATA  
 AGGTTTACCCCTTGATACGGAATTTACACAGGTAGGGAGTGTTTAGTGGACAATAGTGTAGG  
 TTATGGATGGAGGTGTCGTTACTAAATTGAATAACGAGTAAATATCTTACTTGGGTAGAGA  
 TGGCCTTTGCCAACAAAGTGAACCTGTTTTGGTTGTTTTAACTCATGAAGTATGGGTTCACT  
 GGAATATGTTTGAAGCTCTGAAGGATTAGACAAGGTTTTGAAAAGGATAATCATGGGTAGA  
 AGGAAGTGTTTGAAAGTCACTTTGAAAGTAGTTTGGGCCAGCACGGTAGCTCACCTT  
 GGTAAATCCAGCACTTTGGGAGCTTAAGTGGGTAGATTACTTGGCCAGGAATTCAGACCA  
 GCTTGGCAGATGGTGAACCTGTTCTATAAAAATAATCTGGCTTTGAGCATATGCCTCTGGTC  
 CAGCATGAGAGCTAGTGAAGATTGCTGAGCCAGAGCCAAAGTTGCACTGAGCAGCTCA  
 CGTCACTGCACTCTAGCTGGCAGAGTAAGCCAAAAAATATATATATATTGAAATCAAGG  
 AGGCAAAATTTTGACAGGGAAGGAAGTAACTGCAAAACCCTAGGCTTTAGTAGGTACTTAT  
 ATAAAATCTAGTCCAGTTCTCTCATTTAAAAAATGAAGCACTGAAATACAGACTTAAATA  
 GCTCAGATAGCTAATTAGGAAATTTCAAGTTGGCCAAATATAGCATTTCTCTGACATTTAA  
 AAATAATTTCTAATTCAAATACATGCATATTGATTTACACCTCATACTGTGATAATTAATGT  
 GATGTGGATTGCTGGTGTCCAGCATGACCCATAAACAGGTCAGAAGAAATGATGGAATGTTTT  
 AGAATAAACTCCTGCTTCTAGTATACATACACAGTTCAAAAGATGTTTAAATGCTTTTGTAT  
 TTACTGCCATGTAAATGAAATATATAGATTATTGTAACCTTTCAACCTGAAATCAGACAGT  
 ATGAGATTTGATTGTTGTTATGTGTCTACTAGTGTCTAATGAAGCTTTTAAATCTACAATT  
 TCTTCTTTAAAAATATTTTATTAATGTGAATGGAATATAACCAATCAGCTTAAATCCCAACC  
 TTATCTGTGTGTAGACATTTGATTCACAATTTTGAATGGCTGTGTTTACCTCTAAATAA  
 ATGAATTCAGAGAAAAA



**FIGURE 41**

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME  
EQLNKIPGFCENEKGVPCNILVGYSKAVYRLCFGLAMFYLLSLLMIKVKSSSDPRAAVHNG  
FWFFKFAAAIAIIIGAFFIPEGTFTTVWFYVGMAGAFCFILIQVLVLLIDFAHSWNESWVEKM  
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLCVGASVMSI  
LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV  
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH  
RAVDNERDGVYSSFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVWKISSSWIGI  
VLYVWTLVAPLVLTNRDFD

GCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTGNAGCGTTGTGGAGAT  
 GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC  
 CCGTGTTTGCTATGCCGATGCTGTCTAGTGGAACAANTCCACTGTAAGTAGATTGATCTA  
 TGCACTTTTCTGCTTGTGGAGATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG  
 AACAAGTGAATAAGATTCTGGATTTTGTGAGAATGAGAAAGGTGTTGCCCTTGTAACATT  
 TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTGGCTATGTTCTATCTTCTTCT  
 CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGAT  
 TTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

**FIGURE 43**

GTTATTGTGAAC TTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC  
CANGTTTGTGTGGAAGTCCCCGTGTTTGNATGCCGATGCTGTCCTAGTGGAACAANTCC  
ACTGTAATTAGATTGATNTATGCAC TTTNTTGCTTGTGGAGTANGTGTAGCTTGTGTAAT  
GTTGATACCAGGAATGGAAGAACA ACTGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAG  
GTGTTGTCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG  
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG  
AGCTGCAGTGCACAATGGATTTTGGTTTTTTAAATTGCTGCAGCAATTGCAATTATTATTG  
GGGC

**FIGURE 44**

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC  
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATAACCATGTTTGTGTGGAAGTGCCCCGTGT  
TGCTATGCCGATGCTGTCTAGTGGAACAACCTCCACTGTAAC TAGATTGATCTATGCACTT  
TTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC  
GAATAAGATTCTGGATTTTGTGAGAATGAGAAAGGTGTTGCCCTTGTAACATTTTGGTTG  
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTA  
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTT  
CTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

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**FIGURE 45**

GCTGTCCTTAGTGGAACAANTCCAACCTGTAACCTGGATTGATCTATGCACCTTTTCCTTG  
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCCAGGATTGGANGAACAACTGAATA  
AGATTCCCTGGATTTTTGTGAGAAATGAGAAAGGTGTTGTCCCCTGTAACTTTTTGGTTGGC  
TATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTCTTACT  
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCT  
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACTTT  
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACAAC TAGT  
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTGAAAAAATGGAAGAAGGGA  
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA  
GTTGCTATCGTCCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTTCAGAAAACAAGGC  
GTTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

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**FIGURE 46**

CTCGGGCGCGCACAGGCAGCTCGGTTTGCCCTGCGATTGAGCTGCGGGTGC GGGGCCGGCCGGCCCTCTCCAAT  
 GGCAAATGTGTGTGGCTGGAGGCGAGCGCAGGGCTTTCGGCAAGGCATGCGAGTGTTCGACAGCCGGGGCGAG  
 TCCTGTGAAGCAGATGAAAAAGAACATTATTAACGTGTCTATTACGAGGAGCGCCCGCCGGGCTGTGCGC  
 ACTCCCGCGGAACATTTGGCTCCCTCCAGCTCCGAGAGAGGAGAAGAAGAACGGGAAAAGAGGCAGATTAC  
 GTCGTTTCAGGCCAAGTGGACCTGATCGATGGCCCTCCTGAATTTATCAGATATTTGATTTATTAGCGATGCC  
 CCCTGGTTGTGTGTACGCACACACACGTGCACACAAGGCTCTGGCTCGCTTCCCTCCCTCGTTTCCAGCTCC  
 TGGGCGAATCCACATCTCTTTCAACTCTCCGCCGAGGGCGAGCAGGAGCGAGATGTGTGCAATCTCGCAGTG  
 AAGAGGACGAGGGAAGAAACAAAGCCACAGACGCAACTTGAGACTCCCGCATCCCAAAAGAACACAGAT  
 CAGCAAAAAAGAAAGATGGGCCCCCGAGCCTCGTGTCTGTCTGTCTCCGCAACTGTGTTCTCCCTGCTGGG  
 TGAAGCTCGGCCCTTCTGTGCGACCACCGCCTGAAAGGCAGGTTTCAGAGGGACCGCAGGAACATCCGCCCA  
 ACATCATCTCGTGTGCTGACGGACGACAGGATGTGGAGCTGGGTTCCATGCGAGGTGATGAACAAGACCCGGCG  
 ATCATGGAGCAGGGCGGGGCGCACTTCATCAACGCCCTTCGTGACCACACCCATGTGCTGCCCTCAGCCTCCTC  
 CATCCTCACTGGCAAGTACGTCCACAACACACCTACACCAACATAGAGAATGAGAATGCTCCTCGCCCTCCTGGC  
 AGGCACAGCAGAGAGCGCACCTTTGCCGTGTACTCAATAGCACTGGTACCGGACAGACTTTCTTGGGAAG  
 TATCTTAATGAATACAACCGCTCTACGTGCCACCCGGCTGGAAGGAGTGGTCCGACTCTTAAAACTCCCG  
 CTTTTATACTACAGCTGTGTGCGAACGGGGTGAAGAGAACGCGCTCCGACTACTCCAAGGATTACCTCA  
 CAGACCTCATCAACCAATGACAGCGTGTGAGCTTCTTCGCCACGTCCTCAAGAGATGTACCCGCACAGGCCAGCTCTC  
 ATGGTGATCAGCCATGACAGCCCCCAGCCCTGAGGATTACGCCCCACATATTCAGCCTCTTCCCAAAGC  
 ATCTCAGCACATCAGCCGAGCTACAATCAGCGCCCAACCCGGACAACACATGGATCATGGCTACACGGGGC  
 CCATGAAGCCCATCCACATGGAATTCACCAACATGCTCCAGCGGAAGCGCTGACAGACCTCATGTCGGTGGAC  
 GACTCCATGGAGACGATTACAACATGCTGTTGAGACGGCGGAGCTGGACAACAGTACATCGTATACACCGC  
 CGACCACGGTTACCACATCGGCCAGTTTGGCCTGGTGAAGGGAAATCCATGCCATATGAGTTTGACATCAGGG  
 TCCGTTCTACGTGAGGGGCCCAACGTGGAAGCCGGCTGTCTGAATCCCCACATATTCAGCTCTCAACATGACCTG  
 GCGCCACCATCTGGACATTCGAGCCTTGACATACCTGCGGATATGGACGGGAAATCCATCCTCAAGCTGCT  
 GGACACGGAGCGGCCGTGATCGGTTTCACTTGAAGAAAGAGATGAGGGCTGCGCGGAGCTCTTCTTGTGTG  
 AGAGAGCGCAAGCTGCTACACAGAGACATGACAAAGTGAAGCGCCAGGAGGAGAACTTTCTGCCCAAGTAC  
 CAGCGTGTGAAGGACCTGTGTGAGCTGCTGAGTACCAGACGCGCTGAGCAGCTGGGACAGAGTGCAGTGC  
 TGTGGAGGACGCCACGGGAAGCTGAAGCTGCATAGTGAAGGGCCCCATGCGGCTGGCGGCGAGCAGAGCCC  
 TCTCCAACCTCGTGCCCAAGTACTACGGGACGGGCAGCGAGGCCCTGCACCTGTGACAGCGGGGACTACAAGCTC  
 AGCCTGGCGGAGCGCCGGAAAAAATCTTCAAGAGAAGTACAAGCGGCTATGTCCGACATCGCTCCAGCTCCG  
 CTCAGTGGCCATCGAGGTGGAACGGCAGGGGTGTACCACGTAGGCCTGGGTGATGCCGCCAGCCCGAAACCTCA  
 CCAAGCGGCACCTGGCCAGGGGCCCTGAGGACCAAGATGACAAGGATGGTGGGACTTCAGTGGCACTGGAGGC  
 GTGACCGTACTACTCAGCGCCCAACCCCATTAAGTGAACATCGGTGCTACATCCTAGAGAACGACACAGTCCA  
 GTTGACCTCCAGCTGTACAACTCCTGCAGCCTGGAAGACCAACAGCTGCACCTGCACCACGAGATTGAAA  
 CCCTGCGAACAATAAAGAACCTGAGGGAAGTCCGAGTCACTGAAGAAAAAGCGGCCAGAAGATGTGAC  
 TGTCAAAAATCAGTACCACACCCAGCAAAAGGCCGCTCAAGCACAGAGGCTCCAGTCTGCATCCTTTTTCAG  
 GAAAGGCCCTGCAAGAGAAGGACAAGGTGTGGCTGTTGCGGGAGCAGAAGCGCAAGAAGAACTCCGCAAGCTGC  
 TCAAGCGCCTGCGAACAACGACACGTGCAGCATGCCAGGCCTCAGTGTCTTACCCACGACAACAGCAGCATGG  
 CAGAGCGGCGCTTTCTGGACACTGGGGCCTTTCTGTGCTTGACACGCGCCACAATAACAGTACTGGTGAT  
 GAGGACCATCAATGAGACTCATGATTTTCTCTTCTGTGAATTTGCAACTGGCTTCTAGAGTACTTTGATCTCA  
 ACACAGACCCCTACGACATGATGAATGAGTGAACAGCTGGACAGGAGTGTCTTCAACAGCTACACGTACAG  
 CTCATGGAGCTGAGAGCTGCAAGGGTTACAAGCAGTGTAAACCCCGACTCGAAACATGGACCTGGATGGAGG  
 AAGCTATGAGCAATACAGGCAGCTTTCAGCGTCGAAAGTGCCAGAATGAAGAGACTTCTTCCAATCACTGG  
 GACAACTTGGAAGGCTGGGAAGGTTAAAGAAACAACAGAGGTGGACCTCCAAAACATAGAGGCTACCTGAC  
 CTGCACAGGCATGAAAACCATGTGGGTGATTTCCAGCAGACCTGTGCTATTGGCCAGGAGGCTGAGAAGC  
 AAGCAGCACTCTCAGTACACATGACGATTTCTGGAGGATAACACGAGGACAGATTAAGTCTCAGGAAGTCC  
 ATTTTGGCCCTGCTTTTGCTTTGGATTATACCTCACCAGCTGCACAAAATGCATTTTTTTCGTATCAAAAAGTC  
 ACCACTAACCTCCCCAGAAGCTCACAAGGAAAAACGGAGAGCGAGCGGACGAGAGATTTCTTGGAAATTTCT  
 TCCCAAGGGCAAGTCAATTTGGAATTTTTTAAATCATAGGGGAAAAACGACTCTGTTCTAAATCTCTTTATCTT  
 TGGTTTTGTCAAAAGAGGAATTAAGAAGCAGGACAGAGGCAACGTGGAGAGGCTGAAAACAGCTGCAGAGC  
 TTTGACAAATGAGTCACTAGCACAAAAGAGATTGACATTTACCTAGCACTATAAACCTGGTTGCTCTGGAAGAA  
 CTGCCTTCAATTGATATATGTGACTATTTACATGTAATCAACATGGGAAGCTTTTAGGGAACTTAATAGAAAT  
 CCAATTTTCAGGAGTGGTGGTGTCAATAACGCTCTGTGGCCAGTGTAAAGAAAAA

**FIGURE 47**

MGPPSLVLCCLSATVFSLLGGSSAFLSHRLKGRFQDRRNIRPNIIILVLTDDQDVELGSMQ  
VMNKTRRIMEQGGAHFINAFVTTMCCPSRSSILTGYVHNHNTYTNNENCSSPSWQAQHE  
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD  
YSKDYLTDLITNDSVSFFRTSKKMPHRPVL MVISHAAPHGPEDSAPQYSRLFNPASQHITP  
SYNYAPNPDKHWMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT  
YIVYTADHGYHIGQFGLVKGKSMPEFDIRVPFYVRGPNVEAGCLNPHIVLNLIDLAPTILDI  
AGLDIPADMDGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN  
FLPKYQRVKDLCQRAEYQTACEQLGQKWQCVEDATGKLLKHCKGPMRLGGSRALSNLVPKY  
YGQGSEACTCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSV AIEVDGRVYHVGLGDAAQ  
PRNLTKRHWPGAPEDQDDKDGGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKS  
LQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKRPEECDCHKISYHTQHKGRLLKHGSSL  
HPFRKGLQEKDQVLLREQKRKKLRLKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG  
PFCACTSANNTYWCMTINETHNLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL  
HVQLMELRSCKGYQCNPRTNRNMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

**FIGURE 48**

AACAAAGTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA  
GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCAGATCTGGGCCTCCTGGGGAGCACAGCCC  
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTGTGCTGCTGCTGCTGCTGGCCACC  
TGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA  
CCGAGTCCGCCGGGCCAGCCTTGGCCCTTCCGGCGGCGGGGCCACCTGGGAATCTTTCACC  
ATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC  
CCCCGCCACACCCCTCACCACCTCCACCACCACCACCACCCCCACCGCCACCATCCCCGCCA  
CGCTCGCTGAGGCTGCTGTGCGCCGGTGCCTGTGGACAGCAGCTGCCCTGCCCTCCCATCTG  
TTCCCAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG  
GGAACAATAGACTGGGGCTTGCTCCAGTCGATTTGCATGGCATGCCCCAGTGACTATGGC  
AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGCTGAAGGGTTGGGGAGTGGAGAGCAAGG  
GTGCTCTTTCGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCCAGTGAGCCCCAGAAATG  
ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC  
ATCAGGCTGCTGCAGGCCCTTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCCTTTT  
GGTTTGAGAAGGCAGTGTGAGGCTGCACAGTCAATTCATCGGTGCCTTAGTCCAAGAAAAT  
AAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA



**FIGURE 49**

MLGLLGSTALVGWITGA AVAVLLLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRR AQWPFR  
RRGHLGI FHHHRHPGHVSHV PNVGLHHHHHPRHTPHHLHHHHHPHRHHPRHAR

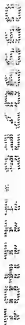
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**FIGURE 50**

GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTGGGGATCCAGAGCC**ATG**TCGGACCTGCTA  
CTACTGGGCTGATTGGGGCCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG  
GTACTCAGGGCTACTGGCTGGGGTGAAGTGAGTGCTGGGTCACCCCCATCCGCAACGTCA  
CTGTGGCCTACAAGTTCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCACTGAGAGC  
TGCAGCATCTCTCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC  
CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC  
CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC  
CATGTGGTGACAGCCACCTTCCCCTACACCACCATTCTGTCCATCTGGCTGGCTACCCGCCG  
TGTCCATCCTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGG  
AGATCTACCAGGAAGACCAGATCCATTTTCATGTGCCCACTGGCACGGCAGGGAGACTTCTAT  
GTGCCTGAGATGAAGGAGACAGAGTGGAATGGCGGGGGCTTGTGGAGGCCATTGACACCCA  
GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGAAGTGAGCC  
CTGGCAGCCGGGAGACTTCAGCTGCCCACTGTACCTGGGGCAGCAGCCGTGGCTGGGAT  
GACGGTGACACCCGAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA  
GGAGCTGGACTTGGAGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCTGGGACTGAGC  
CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCTGAGAAGGGCAAGGAG**TAA**CCC  
ATGGCCTGCACCTCCTGCAGTGCAGTTGCTGAGGAAGTGAAGGAGACTCTCCAGCAGACTCT  
CCAGCCCTCTTCTCCTTCCCTCTGGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCCTGC  
TCCAGGCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCAGGGCCAGAGGAGCCA  
GGGACTATTTTCTGCACCAGCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTC  
ACAGTGAGCTTCCAGGACCCAGAATAAAGCCAATGATTACTTGTTCACCTGGAAAAAAA  
AAAAA

**FIGURE 51**

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGlyGETGR  
LFTESCSISPKLRsIAVYYDNPHMVPPDKRCavgSILSEGEESpSPELIDLYQKFGFKVFS  
FPAPSHVVTATFPYTTILSIWLATRrvHPALDTYIKERKLCAYPRLEIYQEDQIHfMCPLAR  
QGDFYVPemKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSaatLSPGAS  
SRGWDDGDTRSEHSYSESGASGSSFEELDLEGEgPLGESRLDPGTEPLGTTKWLWEPTapeK  
GKE

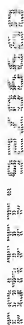


**FIGURE 52**

CCGCGGGAACGCTGTCTGGCTGCCGCCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCT  
 GCCCCGCGCCAGT**CATG**ACCCTGCGCCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCT  
 GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA  
 CCTCCAAGTGGAGACCCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGA  
 GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT  
 GACCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA  
 GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCCTTCTCACTTGGCCTAT  
 GGAAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT  
 GATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTCCTCTGCTGCTG  
 GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAAT  
 AGACCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAA**TA**  
**A**TAAATAATAAATTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

**FIGURE 53**

MTLRPSLLPLHLLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHI  
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLDMCVGEKRRAIIPSHLAYGKRGF  
PPSVPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS  
KKKLKEEKRNSKKK



**FIGURE 54**

CCCGGGAACGTGTTCCCTGGCTGCCGCACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCTGC  
CCCGCGCCAGTCATGACCCCTGCGCCCTCACTCCTCCCGTCCATCTGCTGCTGCTGCTGC  
TGCTCAGTGCGGCGGTGTGCCGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC  
CTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA  
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA  
CCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT  
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTATGG  
AAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGTGCAATGACGTGGAGCTGA  
TTGCACTAATCCGAGCCAACCTACTGGCTAAAGCTGGTGAAGGGCATTITGCTCTGGTAGGG  
ATGGCCATGGTGCCACCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAATAGA  
CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA  
AATAATAAATTTTAAAAAACTTA

**FIGURE 55**

CCGAAAGTCCCGTCCGGACCCTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCC  
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG  
TATTATTGACACCTCCCTGACCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA  
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT  
CCTTCTCACTTGGCCTATGGAAAACGGGGATTTCACCACATCTGTCCCAGCGGATGCAGTGGT  
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACCTACTGGCTAAAGCTGGTGAAGG  
GCATTTTGCCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC  
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA  
CAAGAGCAAAAAGAAATAATAAATAATAAATTTAAAAAACTTAAAA

**FIGURE 56**

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAAATCGGGGGAG  
 TGAGGCGGGCCGGCGCGGCACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG  
 ACCTGAAAAAAATGCTCTGGATTTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG  
 GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGAT  
 TATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCT  
 GTGGTGTATTAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA  
 GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGG  
 TTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTG  
 CTAAAGAAAAAGACATAGTATACCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATCTTT  
 TTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT  
 TTCCCACAGCACAAACAGCCCTGCATGGGTTTGTGTTTTTTTTACTGCTCACTCCCAACCTT  
 TTGTAATGCCATTTTCTAAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT  
 AAAATCACGAGAACACCTAAACAACAACCAAAAATCTATTGTGGTATGCACTTGATTAACCT  
 ATAAAAATGTTAGAGGAACTTTCACATGAATAATTTTTGTCAAATTTTATCATGGTATAATT  
 TGTAAAAATAAAAAGAAATTACAAAAGAAATTATGGATTGTCAATGTAAGTATTTGTCATA  
 TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTTATTCAAATGTGGT  
 CTCTTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTAGTTTTTAAATATTCCGTGG  
 TCAAATTTCTTCTCACTATAATTGGTATTTACTTTTACCAAAAATTTCTGTGAACATGTAAT  
 GTAACTGGCTTTTGAGGGTCTCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT  
 GGTCCAGCCACCAGGCTCCCTGTGTCCCTTCCATGGGAAGGTCTTCGCTGTGCCTCTCATT  
 CCAAGGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC  
 CACATCCACCACTG



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**FIGURE 57**

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIDA AVIYPTMKDFNHSYHACGVI  
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK  
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

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**FIGURE 58**

TTCTTGGCTAAAAATCGGGGGAGTGAGGCGGGCCGGCGCGCGACACCGGGCTCCGGAACC  
ACTGCACGACGGGGCTGGACTGACCTGAAAAAAATGTCTGGATTTCTAGAGGGCTTGAGATG  
CTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC  
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTATTTATCCCACCATGAAAGAT  
TTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGC  
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTG  
CTCGCATTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG  
ATTCTTTTTTGGAGGTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATT  
TTTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGC

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TGGACGGACCTGAAAAAAATGTTTGGATTNTAGAGGNNTTGAGATGTTCAGAATGCATGAC  
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG  
GTGGATTATCATAGATGCAGNTGTTATTATCCCACCATGAAAGATTTCAACCANTCATACC  
ATGCCCTGGTGTTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA  
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTGGGTCAAACAGGTGCTCGCATTTGGCTTTT  
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTT  
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTTCCAGAATGCCTTC  
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

**FIGURE 60**

GGACACCGGGTCCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAATGTTTGGATT  
TTTAGAGGGCTTGAGATGNTCAGAAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT  
CCATTGCTGCTGGTGTACTATTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT  
TATCCCACCATGAAAGATTNAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGC  
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT  
GTTTGGGTCAAACAGGTGNTCGCATTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATT  
CTGATTGNATTCTATGCGGATTCTTCTTGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT  
ACCCTGGAATTNCTNTATTTTTCCAGAATGCC



**FIGURE 61**

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATANTATTGCTTCC  
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT  
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCTGTGGTGTTATAGCAACCATAGCC  
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG  
TTGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN  
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC  
CCTGT

**FIGURE 62**

GGGAGGCTGTGNCCGTTTTGTTTTNTGGCTAAAATCGGGGGAGTGAGGCGGCCCGGCGCGG  
CGNGACACCGGGTTCCGGGAACCATTGCACGACGGGGTGGACTGACCTGAAAAAATGTTTG  
GATTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATT  
GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT  
TATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCA  
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA  
GGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG  
ATNTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG  
TATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

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GTACGCGCGGGTGA**TAGT**GGGCTTCGGCTGGTGCTGCTCCTGGCTGTGCTGCTGCTGGCCGTCC  
TGCTCAAAAGTTTACTTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTC  
AAACGGCCGCCAGCGCCCTGGTAACTGACAAGGAGGCCAGGAAGAAGGTTCTCAAACATGAC  
TTTTTTCAGCCAAACCAAGTCGCCGGAAGAGCTGGATGTGGTGGAATTTGGCATGGCTTTGGGG  
CCCTGGGTGCAGCTGCAATTTCTAGCTAAAGCTGCAAGCGAGTCTGGTGCTGGACAACAT  
ACCAAGGACCGGGGGCTGCTGTCTATACCTTTTGGAAAGATGGCTTTGAATTTGACACGAAT  
CCATTACATTTGGCGGTATGGAAGAGGGCAGCATTTGGCCGTTTTATCTGGACGAGTACTG  
AAGGCGACCTGGAGCTGGGCTCCCCGTCTCTCTCTCTTTGACATCATGGTATGGAAGGGCCC  
AATGCCCGAAAGGATACCCCATGTACAGTGGAGAGAAGGCCATACATTACGGCTCTCAAGGG  
GAAGTTTCCACAGGGAAGCTATCATTGACAAGTATATAAAGCTGGTTAAGGTGGTATCC  
GTGGAGCCCTCATGCCATCTGTTCAAATTCCTCCATTGCCGTGGTTTCAGCTCTCGAC  
AGGTGTGGGCTGCTGACTCGTTTTCTCTCATTCCTTCAAGCATACCCAGAGCGCTGGCTGA  
GGTCTCTCAGCAGCTGGGGGCCCTCTGAGTCTCAGGCGAGTACTCAGTACATCTTCCCCA  
CTTACGGTGTACCCCCAACACAGTGCCTTTTCATGACCGCCCTGCTGGTGCAACCATAC  
ATGAAGAGGAGGCTTTTATCCCCGAGGGGTTCCAGTGAATTCGCTTCCACCATCCCTGTT  
GATTACGCGGGCTGGGGCGCTGTCTCTACAAAGGCCATGTGACAGTGTGTTGCTGGCT  
CAGCTGGGAAAGCCTGTGGTGTTCAGTGTGAAGAAGGGGCATGAGTGGTGAACATCTATTGC  
CCCATCTGGTGTCTCAACCGAGGACTGTTCAACACCTATGAACACCTACTGCCGGGAAGCG  
CCGCTGCCCTGCCAGGTGTGAAGCAGCAACTGGGACGCTGCCGGCCGGTGTAGGCATGACT  
TGTTTTCTATCTGCTGGAGGCCAACGAAGAACCTGCATCTGCCCTCACCACTACTAT  
GGTTACTGACACCGGCATGTACAGGCGCATGGACGGCTACGTTCTCCATGCCAGGGAAGA  
GGTCTCGGAACACATCCCTCTTCTCTTCCGCTTCCCATCAGCCAAAGATCCGACCTGGG  
AGGACCGATTTCCAGGCGGGTCCACCATGATCATGCTCATACCCACTGCCACGAGTGGTT  
GAGGAGTGAGCGAGGCGGAGCTGAAGGGAAAGCGGGGACGTGACTATGAGACCTTCAAAAAT  
TTTTTGTGGAAGCTCTATGTGAGTGTCTGAAATCTTCCACAGCTGGAGGGGAAGGTGG  
AGAGTGTGGCTGACGATCCCCACTACCAACAGCACTTCTATCTGGTGTCTCCCCAGGTGCC  
TGCTATGAGGCTGACCATGACCTGGGCGCGCTGCACCTTGTGTGATGGCCTCTTGAGGCC  
CCAGAGCCGCATCCCCAACCTCTATGTACAGCGCCAGGATATCTTCACTGTGGAATGTGTG  
GGGCGCTGCAAGGTGCCCTGCTGTGTGACGAGCGGCATCTGAAGCGGAAGTTGTACTACG  
CCTAAGAACTTTGATTTAGGATCGGGGACAGAGAAGAAAAGAT**TAGT**TCCATCAGGAGG  
ATTGACAGGAATTTGCCAATGGCTGGGCATCTCCCTTGACTTACCCATAATGCTTCTTG  
CATTAGTGTCTTGACAGGTATAAAGCACTCAATTTGGTTCTGTAGTCTGAAGAGGGCCTAG  
TTTTAAATCACAATTCGGAATCTGGGGCAATGGAATCAGTCTTCCAGCTGGGCGAGTGGAT  
TCTTTACGCGCTTTTATAACATGCCATCCCTAATAGATATTTGACTTGGATAGCTGTGATG  
TCTCATGACGAGCGCGCTCTGTGATCCCTCCACCATCGCTCCTTAATCATGTTGATCAAAGCGA  
ATATTCCATCTGTGGATAGAACCCTGGCAGTGTGTGACGTCAACCTGGTGGGTTCAGTGT  
TGCTCTGAGGCTCTGTCTCTCATTTAGTCTACCTGTGACAGTGTCTACACTGTCAAGG  
GAAAAGGAGACTAATGAGGCTTAACTCAAACCACTGGGCGTGTTTTGGTTGCCATTTCCATA  
GGTTTGGAGAGCTCTAGATCTCTTTTGTGCTGGTGTACAGGGTCTTCAAGGACAGGAAT  
GCCGTGTCTTGGCCAGTGTGGTTCTGGAGCTTTGGGGTCAAGCAGGATCCATCAGTTAGTA  
GGGTGCATGTTCAGATGATCATCAAAATCATATGGAAGTCCGGGCTGTCTTCTTTATCA  
TCGGGGTGGCAGCTGGTTCTCAATGTGCCAGGGGACTCAGTACCTGAGCTCAATCAACG  
CTTATCCACCAATACACAGGGAAGGGTGATGCAGGGGAAGGGTGACATCAGGAGTCAGGGCA  
TGACATGTGAAGTATGAATCTTTGTGGGCTGAAGCAGGCTCAGGGGCATTCAGCCCAAGG  
CACAGCAGGGGACAGTGCAGGAGGTTGGGGTAAAGGAGGGAAGTCACATCAAGAAAAGGA  
AAGCCAGCGGAATGTGTGTGAAGCCCCAGAATGGCATTTGCAAGTTAATAGCACATGTAGGG  
TTAGACAGGTAGTGAATGCACAGCTCAAGGTTTTGAAAAATGACTTTTCAGTATGTCTTTG  
GTATCAGACATACGAAGAGTCTCTTTGTAGTTCTGTGTTAATGTAACATTAAATAAATTTATTG  
ATTCCTATTCGTTTTAAAAAAAAAAAAAA

**FIGURE 64**

MWLPLVLLLA VLLLA VLCKVYLGLFSGSSPNPFSE DVKRPPAPLVTDKEARKKVLKQAFSAN  
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG  
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQ  
EEAII DKYIKLVKVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ  
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPVIQRA  
GGAVLT KATVQSVLLDSAGKACGVSVKKGHELVNIYCPIVVSNAGLFNTYEHLLPGNARCLP  
GVKQQLGTVRPGLGMTSVFICLRGTKEDLHLPSTNYVYVYDMDQAMERYVSMFREEAAEH  
IPLLFFAFPSAKDPTWEDRFPGRSTMIMLIPTAYEWFEWQAE LKGKRGSDYETFKNSFVEA  
SMSVVLKLFQLE GKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI  
PNLYLTGQDIFTCGLVGALQ GALLCSSAILKRNLYS DLKNLDSRIRAQKKKN



**FIGURE 65**

GCAGCGGCGAGGCGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCTA  
 GGGGTTGGCACCGGCCCGAGAGGAGGATGCGGGTCCGGATAGGGCTGACGCTGCTGCTGTG  
 TGCGGTGCTGCTGAGCTTGGCCTCGGCGTCCCTCGGATGAAGAAGGCAGCCAGGATGAATCCT  
 TAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTAAAGGACCATACTACTGCAGGCAGA  
 GTAGTTGCTGGTCAAATATTTCTTGATTGAGAAGATCTGAATTAGAATCCTCTATTCAAGA  
 AGAGGAAGACAGCCTCAAGAGCCAAGAGGGGAAAGTGTACAGAAGATATCAGCTTTCTAG  
 AGTCTCCAAATCCAGAAAACAAGGACTATGAAGAGCCAAAGAAAGTACGGAACCAGCTTTG  
 ACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCTTTTCTTAGATAA  
 GGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTGCTACAACCT  
 ATGACTACAAGCAGATGAAAAGTGGGGCTTTTGTGAACTGAAGAAGAGGCTGCTAAGAGA  
 CGGCAGATGCAGGAAGCAGAAATGATGTATCAAACCTGGAATGAAAATCCTTAATGGAAGCAA  
 TAAGAAAAGCCAAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA  
 CCAAAGCCCTGGAGAGAGTGTATATGCTCTTTTATTTGGTGATTACTTGCCACAGAATATC  
 CAGGCAGCGAGAGAGATGTTTGAGAAGCTGACTGAGGAAGGCTCTCCCAAGGGACAGACTGC  
 TCTTGGCTTTCTGTATGCCTCTGGACTTGGTGTTAATTCAGTCAGGCAAAGGCTCTTGAT  
 ATTATACATTTGGAGCTCTTGGGGCAATCTAATAGCCACATGGTTTTGGTAAGTAGACTT  
TAGTGGAAGGCTAATAATATTAACATCAGAAGAATTTGTGGTTTTATAGCGGCCACAACTTTT  
 TCAGCTTTCATGATCCAGATTTGCTTGTATTAAGACCAAATATTCAGTTGAACCTCCTTCAA  
 ATTCTTGTTAATGGATATAACACATGGAATCTACATGTAATGAAGTTGGTGGAGTCCACA  
 ATTTTTCTTTAAATGATTAGTTTGGCTGATTGCCCTAAAAAGAGAGATCTGATAAATGGC  
 TCTTTTTAAATTTCTCTGAGTTGGAATTGTGAGAATCATTTTTTACATTAGATTATCATAA  
 TTTTAAAAATTTTCTTTAGTTTTTCAAATTTTGTAATGGTGGCTATAGAAAAACAACAT  
 GAAATATTATACAATATTTGCAACAATGCCCTAAGAATTGTTAAATTCATGGAGTTATTT  
 GTGCAGAATGACTCCAGAGAGCTCTACTTTCTGTTTTTACTTTTCATGATTGGCTGTCTTC  
 CCATTTATTCTGGTCATTTATTGCTAGTGACACTGTGCCTGCTTCCAGTAGTCTCATTTTCC  
 CTATTTTGCTAATTTGTTACTTTTTCTTTGCTAATTTGGAAGATTAACTCATTTTAAATAAA  
 ATTATGTCTAAGATTAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAA

MRVRIGLTLLLCVALLSLASASSDEEGSQDESLSKTTLTSDSEVKDHTTAGRVVAGQIFLD  
SESELESSIQEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKKVRKPALTAIEGTAHG  
EPCHFPFLFLDKKEYDECTSDGREDDRLWCATTYDYKADEKWGFCETEEEAARRQMQEAEEM  
YQTGMKILNGSNKKSQKREARYLQKAASMNHTKALERSVYALLFGDYLPQNIQAAREMFEK  
LTEEGSPKQGATALFLYASGLGVNSSQAKALVYTFGALGGNLIAMHVLVSRL

**FIGURE 67**

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT  
GCCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCT  
GTCAGTTTCCCAGACAGTCTTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG  
CTCAACTCTCCTGCACGCTCAGCCCCCAGCACGTCACCATCAGGGACTACGGTGTGTCTCTGG  
TACCAGCAGCGGGCAGGCAGTGCCCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA  
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAAATGCCT  
GTGTCCCTCACCATTAGTCCCGTCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTGGC  
TACGGCTTTAGTCCCTAGGGGTGGGGTGTGAGATGGGTGCCCTCCCCTCTGCCCTCCATTCT  
GCCCTGACCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAAATGGG  
TTAATAATATTCAACATGTCAACAAC

**FIGURE 68**

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPQQAQLSCTLSPQHVTIRDYGVSWYQQRAG  
SAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVPEDDADYYCSVGYGFS

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**FIGURE 69**

GCGGCCCCGCCCCGAGACCGGGCCCCGGGGCGCGGGGCGCGGGATGCGGCGCCCCGGGGCGG  
 CGATGACCGCGGAGGCGCACGCGCGGGCCCCGGCCCTGACCCCGCCGCCGCCCGCTGAGCCCC  
 CCGCGCAGGTCCGAGACAGGCGGAGATGACGCCAGCCCTGTTGCTGCTCTGCTGCCGCG  
 CGCTGCTGCTGGGGGCGCTTCCACACCGGCCGCCGCGCCCGAGGCCCCCAAGATGGCGGAC  
 AAGGTGGTCCACGCGAGGTGGCCCGGCTGGGCGGCACTGTGCGGCTGCAGTGCCCAAGTGA  
 GGGGACCCGCGCCCGCTGACCATGTGGACCAAGGATGGCCGACCATCCACAGCGGCTGGA  
 GCGGCTTCCGCGTGTGCGCGAGGGGCTGAAGGTGAAGCAGGTGGAGCGGGAGGATGCCGCG  
 GTGTACGTGTGCAAGGCCACCAACGGCTTCGGCAGCCTGAGCGTCAACTACACCCCTCGTCGT  
 GCTGGATGACATTAGCCCAGGGAAGGAGAGCCTGGGGCCCGACAGCTCCTCTGGGGGTCAAG  
 AGGACCCCGCCAGCCAGCTGGGCACGACCGCGCTTCACACAGCCCTCCAAGATGAGGCGC  
 CGGGTGATCGCACGCCCCGTGGGTAGCTCCGTGCGGCTCAAGTGCCTGGCCAGCGGGCACC  
 TCGGCGGACATCAGCTGGATGAAGGACGACACGGCTTCAGCGCCAGAGCCCGCTGAGC  
 CCAGGAAGAAAGTGGACACTGAGCCTGAGAACCCTGCGCGCGGAGGACAGCGGCAAAATAC  
 ACCTGCCCCTGTGTCAACCGCGCGGGCGCCATCAACGCCACCTACAAGGTGGATGTGATCCA  
 CGGACCCGTTCCAAGCCCGTGTCTACAGGCACGACCCCGTGAACACGACGGTGGACTTCG  
 GGGGACCCAGTCTCTCCAGTGCAAGGTGCGCAGCGACGTGAAGCCGGTGATCCAGTGGGTG  
 AAGCGCGTGGATAGCGCGCGGAGGGCGGCCACAACCTCACCATCGATGTGGGCGGCCGAA  
 GTTTGTGGTGCTGCCACCGGTGACGTGTGGTGCGGCCCGACGGCTCCTACCTCAATAAGC  
 TGCTCATCACCGGTGCCCGCGGAGACGATGCGGGCATGTACATGTGCTTGGCGCCAAACC  
 ATGGGCTACAGCTTCGCGAGCGCCTTCTCACCCTGCTGCCAGACCCAAAACCGCCAGGGCC  
 ACCTGTGGCCTCCTCGTCTCGGCCACTAGCCTGCCGTGGCCGTGGTCTCATCGGCATCCGAC  
 CCGCGCTGTCTTATCCTTGGGACCCCTGCTCCTGTGGCTTTGCCAGGCCCCAGAAAGCCG  
 TGCACCCCGCGCCTGCCCTCCCCCTGCCCTGGGCACCGCCCGCGGGGACGGCCCGCGACCG  
 CAGCGGAGACAAGGACCTTCCCTCGTTGGCCGCCCCCAGCGCTGGCCCTGGTGTGGGGCTGT  
 GTGAGGAGCATGGGTCTCCGCGAGCCCCCGAGCACTTACTGGGCCCCAGGCCAGTTGCTGGC  
 CCTAAGTTGTACCCCAAACCTCTACACAGACATCCACACACACACACACACACTCTCACAC  
 ACATCTCACAGCTGGAGGGGCAAGGTCCACCAGCACATCCACTACAGTGTAGACGGCACCGT  
 ATCTGCAGTGGGCACGCGGGCGCGGCAGACAGGCAGACTGGGAGGATGGAGGACGGAGCT  
 GCAGACGAAGGCAGGGGACCCATGGCCAGGAGGAATGGCCAGCACCCCGAGGACGTCTGTGTG  
 TGAGGCATAGCCCCCTGGACACACACACACAGACACACACTACCTGGATGCATGTATGCAC  
 ACACATGCGGCGCACAGTGTCTTGAAGGCACAGTACCCACACGACACATGCACAGATATG  
 CCGCTGGGCACACAGATAGCTGCCAAATGCACGCACACGCACAGAGACATGCCAGACA  
 TACAAGGACATGCTGCCTGAACATACACACGCACACCCATGCGCAGATGTGCTGCCCTGGACA  
 CACACACACACACGGATATGCTGTCTGGACGCACACACGTGCAGATATGGTATCCGGACACA  
 CACGTGCACAGATATGCTGCCCTGGACACACAGATAATGCTGCCTTGACACACACATGCACGG  
 ATATGCTTGGACACACACACACACACACGCGTGCACAGATATGCTGTCTGGACACGCACAC  
 ACATGCAGATATGCTGCCCTGGACACACACTTCCAGACACAGTGCACAGGCGCAGATATGCT  
 GCCTGGACACACGAGATATGCTGTCTAGTCACACACACACGACAGATATGCTGTCCGGACAC  
 ACACACGCATGCACAGATATGCTGTCCGGACACACACGACGCAGATATGCTGCCCTGGAC  
 ACACACACAGATAATGCTGCCCTCAACACTCACACACGTGCAGATATGCTTGGGTGCCACACA  
 TGTGCACAGATATGCTGTCTGGACATGCACACAGTGCAGATATGCTGTCCGGATACACACG  
 CAGCACACATGCAGATATGCTGCCCTGGGACACACTTCCGGACACACATGCACACACAGGT  
 GCAGATATGCTGCCCTGGACACACACAGATAATGCTGCCCTCAACACTCACACACGTCGAGA  
 TATTGCTTGGACACACACTGTGCACAGATATGCTGTCTGGACATGCACACAGTGCAGATA  
 TGCTGTCCGGATACACACGCACACACATGCAGATATGCTGCCCTGGGACACACTTCCGGGA  
 CACACATGCACACACAGGTGCAGATATGCTGCCCTGGACACAGCAGACTGACGTGCTTTTGG  
 GAGGGTGTCCGCTGAAGCTGCGAGTACGTGTGCCGTGAGGCTCATAGTTGATGAGGGACTTT  
 CCGTGCTCCACCTGACTCCGCCAACTCTGCCCGCCTGTGTCCCGCCTAGTCCCAGCCTC  
 CATCCCGCCTCTGTCCCTGCCCTTGGCGGCTATTTTGGCCAGTGCCTTGGGTGCCCAGG  
 AGTCCCCCTACTGCTGTGGGCTGGGCTGGGGGACAGACGCCCAAGCCTGAGAGGCTGGAG  
 CCGATGGCTAGTGGCTCATCCCACTGTCATTTCCCTGACAGAGAAGGGGCTTGGTA  
 TTTATATTTAAGAAATGAAGATAATATTAATAATATGGAAGAGAACCTGGGTTCAGAGGAC  
 TGTGGTCTCTCTGGGGGCGGGGACCCGCGCTGGTCTTTACGCCATGCTGATGACCACACCC  
 GTCCAGGCCAGACACCACCCCAACCCCACTGTGCTGGTGGCCCCAGATCTCTGTAATTTTA  
 TGTAGAGTTTGAGCTGAAGCCCCGTATATTTAATTTATTTTGTAAACAAAA

**FIGURE 70**

MTPSPLLLLLLPLLLLGAFPPAAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPPLTM  
WTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGLSVNYTLVVLDDISPGK  
ESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIA RPVGSSVRLKCVASGHPRPDITWMK  
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTRSKPVL  
TGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFVVLPETGD  
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPKPPGPPVASSSSA  
TSLPWPVVIGIPAGAVFILGTL LLWLCAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPS  
LAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTHSHTHSHVEGKV  
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**FIGURE 72**

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESPGEWTTWFNI  
 DYPGGKG DYERLDAIRFYYGDRVCARPLRLEARTTDWTPAGSTGQVVHGSPREGFWCLNREQ  
 RPGQNC SNYTVRFLCPPGSLRRDTERIWS PWS PWSKCSAACGQTGVQTRTRICLAEMVSLCS  
 EASEEGQHCMGQDCTACDLTCFPMQV NADC DACMCQDFMLHGAVSLPGGAPASGA AIYLLTK  
 TPKLLTQTDS DGRFRIPGLCPDGK SILKITKVKFAPIVL TMPKTS LKAATIKAEFVRAETPY  
 MVMNPETKARRAGQSVSLCCKATGKPRPD KYFWYHNDTLLDPSLYKHESKLVLRLQHQAG  
 EYFCKAQSDAGAVKSKVAQLIVTASDETPCNFVPESYLIRLPHDCFQ NATNSFY YDVGRCPV  
 KTCAGQQDNGIRCRDAVQNC CGISKTEERE IQCSGYTLPTKVAKECSCQRCTETRSIVRGRV  
 SAADNGEPMRFGHVYMGNSRVSM TGYKGTFTLHVPQDTERLVLT FVDRLQKFVNTTKVLPFN  
 KKGSAVFHEIKMLRRKEPIT LEAMETNII PLGEVVGEDPMAELEIPSR SFYRQNGEPYIGKV  
 KASVTFLDP RNISTATAAQ TDLNFINDEGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHL  
 DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNL  
 DVPESRRCFVKV RAYRSERFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA  
 CVPAFCDQDQSPDAYSAYVLASLAGEELQAVESSPKFNPN AIGVPQPYLNKLN YRRTDHEDPR  
 VKKTAFAQISMAKPRPNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDNTVFFN  
 EDDPMSWTE DYLAWWPKPMEFRACYIKVKIVGPLEVNVR SRNMGGTHRRTVGKLYGIRDVRS  
 TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTL VKVIPQGSRRASVNPMLHEYLVNHLPLAV  
 NNDTSEYTMLAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTSDGSSRIMKSNVGVALT  
 FNCVERQVGRQSAFYQLQSTPAQSPAAGTVQGRVPSRRQQRASRGGRQGGVVASLRFPRVA  
 QQPLIN



**FIGURE 73**

CTGCAAGTTGTTAACGCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCCTCAATATACCTGAATACGCAC  
 AATATCTTAACTCTTCATATTTGGGTTTTGGGATCTGCTTTGAGGTCCCATCTTCATTTAAAAAAAATACAGAG  
 ACCTACCTACCCGTACGCATACATACATATGTATATATATGTAACCTAGACAAGATCGCAGATCATAAAGC  
 AAGCTCTGCTTGTATTTCCAAGAAGATTACAAGAATTATAGAGAGTGATTTGTCAAGATCCCTGTCGATTTCATG  
 CCCTTTGGGTTACGGTGTCCTCAGTGATGCAGCCCTACCCCTTTGGTTTGGGGACATTATGATTGTGTAAAGACT  
 CAGATTTCACCGAAGAAGGGAAAGTTTGGGATTACATGGCCTGCCAGCCGGAATCCACGGACATGACAAAATA  
 TCTGAAAGTGAAACTCGATCCTCCGGATATTACCTGTGGAGACCCCTCCTGAGACGTTCTGTGCAATGGGCAATC  
 CCTACATGTGCAATAATGAGTGTGATGCCAGTACCCCTGAGCTGGCACACCCCCCTGAGCTGATGTTTGTATTTT  
 GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTGGAAAGGAGTATCCCAAGCCCTCTCCAGGTTAAACAT  
 CACTCTGTCTTGGAGCAAAACCATTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACC  
 AAATGATCCTGGAGAAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATATGCCACAGACTGCTTA  
 GATGCTTTTCACATGGATCCTAAATCCGTGAAGGATTATCAACAGCATACGGTCTTAGAAAAATCATTGCAAGA  
 AGAGTACTCAACAGGTATACAACAAATAGCAAAATAATCCACTTTGAAATCAAAGACAGGTTCCGCGCTTTTGT  
 CTGGACCTCGCCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAACCAAGAAACTCAGAGATTCTTTT  
 ACAGTCACAGACTGAGGATAAGGCTGTTAAGACCAAGCCGTTGGGGAAATATTTGTAGATGAGCTACACTTGGC  
 AGCTACTTTTACGCGATTCTCAGACATAAAGGTCCGAGGAAGTGCAAGTGTAACTCCATGCCACTGTATGTG  
 TGTATGACAACAGCAAAATGACATGCGAATGTGAGCACAAACATACAGGTCCAGACTGTGGGAAATGCAAGAAG  
 AATATCAGGGCCGACCTTGGAGTCCAGGCTCCTATCTCCCCATCCCCAAGGCACTGCAAAATACCTGTATCCC  
 CAGTATTTCCAGTATTTGGTACGAATGTCTGCGACAACGAGCTCCTGCATGCCAGAACGGAGGGACGTGCCACA  
 ACAACGTGCGCTGCGCTGTGCCCCGGCCGCATACACGGGCATCCTCTGCAGAAAGCTGCGGTGCGAGGAGGCTGGC  
 AGCTGCGGCTCCGACTCTGGCCAGGGCGCGCCCCGACGGCACCCACGCGTGTGCTGTGCTGACCACGCTGCT  
 GGGAAACGCCACGCCCTGGTGTCTTAGTGTGTACCTCCAGCCACACCGGACGGGCGCTGTGCGCTGGGGAAGCA  
 GACACAACCCAAACATTGTGCTACTAACATAGGAACACACACATACAGACACCCCTCAGACAGTGTACAAA  
 CTAAGAAGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGAGTCAAGACTGTTAATTTT  
 TGACTCCAGAGGAGTTGGCAGCTGTTGATATTTTACTGCAAAATCACATTGCCAGCTGCAGAGCATATTTGTGGA  
 TTGGAAGAGCTGCGACAGCCCCCAACAGGAAGACAAAACAAACAAATCAACCCGACCTAAAAACATTGGC  
 TACTCTAGCTGTGTGCGCCCTAGTACGACTCCGCCAGTGTGTGGACCAACCAATAGCAATCTTTGCTGTGAG  
 GTGCTATTGTGGGCATAAAGGAATCTGTTACAAGCTGCCATATTGGCTGCTTCCGTCCTGAAATCCCTTCCAAC  
 CTGTGCTTTAGTGAACGTGCTCTGTAAACCTCGTTGGTTGAAGATTTCCTTGTCTGATGTTAGTGATGCACA  
 TGTGTAAACGCCCTCTAAAAGCGCAAGCCAGTATACCCCTGTATATCTGATGAGCACTGATGTCAGCAATG  
 GCACACACCCACTATACAAGAGTGGCTATAGGAAAAAGAAAGTGTATCTATCCTTTGTATTCAAATGAAGTT  
 ATTTTCTTGAACCTACTGTAATATGTAGATTTTTTGTATTATTGCCAATTTGTGTTACCAGACAATCTGTTAAT  
 GTATCTAATTCGAATCAGCAAGACTGACATTTTATTGTCTCTTTCGTTCTGTTTGTTCATCTGCGAGA  
 GATTTCTCTGTAAGGGCAACGAACGTGCTGGCATCAAAGAATATCAGTTTACATATATAACAAGGTAAATAAGA  
 TTCCACCAAAAGGACATTCTAAATGTTTTCTTGTGCTTTAACACTGGAAGATTAAAGAATAAAAACTCCTGCA  
 TAAACGATTTTCAGGAATTTGTATTGCAATTTCTTAAGATGAAGGAACAGCCACCAAGCAGTTTCACACTCACT  
 TTACTGATTTCTGTGGAGTGAATACATTGAGTGAACGAATTAGTTCCAGGAAGATGGATTGATGTTCACT  
 AGCTTGGACAACCTCTGCAAAATATGAGACTATTTCCACTTGGGAAAAATTACACAGCAAAAAAAAAAAAAA  
 AAAAAA

**FIGURE 74**

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK  
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK  
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMLEKSLDYGRTWQPYQYYATDCLDAF  
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD  
TTKKLRDFFTVDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN  
SKLTCECEHNTTGPDCKGCKKNYQGRPWSPGSYLPPIPKGTANTCIPSISISIGTNVCDNELLH  
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTTLLGTAS  
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**FIGURE 75**

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTGCGCTAAGATTGCTGAGGAGCGG  
 CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCCGCTCCGGGCGAGGTGTCTCATGACTT  
 CTCTTGTGGACC**ATG**TCCGTGATCTTTTTGCCTGCGTGGTACGGGTAAAGGATGGACTGCC  
 CCTCTCAGCCTCTACTGATTTTTACCACACCCAAGATTTTTTGAATGGAGGAGACGGCTCA  
 AGAGTTTAGCCTTGCAGCTGGCCAGTATCCAGGTCGAGGTTCTGCAGAAGGTTGTGACTTT  
 AGTATACATTTTTCTTCTTTCCGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGCTC  
 AGCAGCCATGGCCTTCTGCTTCCTGGAGACCCTGTGGTGGGAATTCACAGCTTCCTATGACA  
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTACAG  
 AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGAAAAAAT  
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA  
 ATGGGGTGATGAATGGTCACACACCGATGCACCTGGAGCCTGCTCCTAATTTCCGAATGGAA  
 CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTCTCAACATCATGTGTGCTGCCCTGAATCT  
 CATTCGAGGAGTTCACCTTGCGAACATTCTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT  
 TGGACCAAACCTCG**TGA**GCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT  
 CCGGGAGCAGTGATGTCAAACCTTCTGCTGCTGGGGAAATCTCATCAGCAGGGAGCCTGTGGA  
 AAAGGGCATGTCAAGTAAATCTGGGAATGGCTGGATTGCGAAACATCTGCCCATGTGTATTG  
 ATGGCAGAGCTGTTGCCCAACAAGCGCCTTTTATTTAGGGTAAATTAACAAATCCATTCTAT  
 TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCCTTACATTTATATGATTCTGGGGTT  
 GCTTCAGAAGTGTTATTTTCATGAATCATTATATGATTTGATCCCCAGGATTCTATTTTGT  
 TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTTAGTCAGGGCAAACCAT  
 TTACTTTACATATTCGTTTTCAATACTTGCTGTTTCATGTTACACAAGCTTCTTACGGTTTTT  
 TTGTAACAATAAATATTTTGAGTAAATAATGGGTACATTTTAACAACTCAGTAGTACAACC  
 TAACTTGTATAAAAGTGTGTAATAATGTATAGCCATTTATATCCTATGTATAAATTAATG  
 AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTATTAAAAAAAAAAAAAAAAAAAA  
 AAAAG

**FIGURE 76**

MSVIFFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFS IHF  
SSFGDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQKVW  
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEFAPNFRMEPVTA  
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

**FIGURE 77**

TGCTTCCTGGAGACCCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT  
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAGAAAGTGAAGTGGCATT  
TTAACTATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGGA AAAAATTCAGGAGGAGCTCAAG  
TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT



**FIGURE 79**

MEAPDYEVL SVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATV NK  
IALELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYIQLNGSLIHGLWNLVFLFPNLSL  
IFLMPFAYFFTESEGFAGSRKGVLRVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL  
YDFWEYYLPYLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLEEDLEEQLYCSAFEE  
AALTRRICNPTSCWLPLDMELLHRQVLALQTQRVLLLEKRRKASAWQRNLGYPLAMLCLLVLT  
GLSVLIVAIHILELLIDEAAMPGRMQGTSLGQVSFSKLGSGFAGVIQVVLIFYLMVSSVVGIFY  
SSPLFRSLRPRWHDAMTQIIGNCVCLLVLSALPVFSRTLGLTRFDLLGDFGRFNWLGIFY  
IVFLYNAAFAGLTTLCVLKTTAAVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ

**FIGURE 80**

GGCTGCCGAGGGAAGGCCCTTGGGTTGGTCTTGGTTGCTTGGCGGCGGCGGNTTCNTCCCC  
GCTCGTCCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC  
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGTGTA  
TTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC  
AAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCG

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**FIGURE 81**

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAAACGAGGCGGTGGTGC  
CTGCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTC  
TGTCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGGCGGCTTCCT  
CCCCGTGTCNTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA  
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCCGAGT  
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC  
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC  
GCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCTCTGCTCCTGCCCTTCT  
CCATCATCAGCAATGAGGTGCTGCACTCCC

**FIGURE 82**

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT  
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTCATGCTGCTGT  
GGGTGATATTACTGGTCCTGGCTCCTGTCACTGGACAGTTTGCAAGGACACCCAGGCCCAT  
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCCTCACTTGCAA  
GGGATTCGCTTCTACTCACCACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA  
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTCAAGGAATCTGGAGAGTACAGATGCCAG  
GCCCAGGGCTCCCTCTCAGTAGCCCTGTGCACTTGGATTTTTCTTCAGAGATGGGATTTCC  
TCATGCTGCCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACCTTAGGCCTCTC  
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTCTGTGTTGAAGGAGAC  
TCTGTGGTTCTGAGGTGCCGGGCAAAGGCGGAAGTAACACTGAATAATACTATTTACAAGAA  
TGATAATGTCCTGGCATTCTTAATAAAAGAACTGACTTCAAAAAAAAAAAAAAAAAAAAAA  
AAA

**FIGURE 83**

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQGTKWYHRYL  
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLD FSSEMGFPHAAQANVELLGSSDLLT

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**FIGURE 84**

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGAGACCCCCGCGCCCCCGGTGT  
 GAGGCGGCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGGCGGAGGAGGCTGTGAG  
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAACCATGGCTCCGCAGAACCTGAGCACCTTTT  
 GCCTGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTG  
 GGGTGCCTCGAAGTGCCTCTATAAAGGATATTAAAAAGGCCTATAGGAACTAGCCCTGCA  
 GCTTCATCCCGACCGGAACCTGATGATCCACAAGCCCAGGAGAAATTCCAGGATCTGGGTG  
 CTGCTTATGAGGTTCTGTGATAGTGAGAAACGGAAACAGTACGATACCTTATGGTGAAGAA  
 GGATTAAAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTTCACACTTCTTTGGGGATT  
 TGGTTTCATGTTTGAGGAACCCCTCGTCAGCAAGACAGAAATATTCCAAGAGGAAGTGATA  
 TTATTTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT  
 AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTGCGCAAGAGAT  
 GCGGACCACCCAGCTGGGCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT  
 GCCCTAATGTCAAAGTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG  
 AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG  
 AGATTTACGGTTCCGAATCAAAGTTGTCAAGCACCAATATTTGAAAGGAGAGGAGATGATT  
 TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT  
 CACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACCGGCCAGGAGCGAAGCT  
 ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA  
 TCACCTTTTGATGTGGATTTTCCAAAAGAAGGTTAACAGAGGAAGCGAGAGAAGGTATCAAA  
 CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTG  
 AATAAAATTGACTTTGTTTTAAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT  
 TTGTGTGTGTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGA  
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTGTGCATTCGGAAAAGAATGACC  
 AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGTGCCGCTGAGT  
 TTCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA  
 GTTGTTAGCAATTTCATTCAAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTG  
 TTATTTTTTA

## **FIGURE 85**

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKLALQLHPDRNPDDPQ  
AQEKFQDLGAAYEVLSDSEKRRQYDITYGEEGLKDGHQSSHGDI FSHFFGDFGFMFGGTPRQQ  
DRNIPRGSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ  
MTQEVVCDECPNVKLVNEERTLEVEIEPGVRDGMETPFIFEGEPHVDGEPGDLRFRIKVVKH  
PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGLPNFD  
NNNIKGLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **Cell attachment sequence.**

amino acids 254-257

#### **Nt-dnaJ domain signature.**

amino acids 67-87

#### **Homologous region to Nt-dnaJ domain proteins.**

amino acids 26-58

#### **N-glycosylation site.**

amino acids 5-9, 261-265

#### **Tyrosine kinase phosphorylation site.**

amino acids 253-260

#### **N-myristoylation site.**

amino acids 18-24, 31-37, 93-99, 215-221

#### **Amidation site.**

amino acids 164-168

**FIGURE 86**

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA  
GCGGCGGGCGGAGGAGTTTTTGAGGATTTTTTGAACAGGACCCGGACAGAGGAACCATGGTT  
CCGCAGAACNTGAGCACNTTTGCCTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG  
ACGAGATTTNTATAAGATTTTGGGGTGCCTNAAAGTGCCTTNTATAAAGGATATTAAGG  
CCTATAGGAAACTAGCCCTGCAGNTTATCCCGACCGGAACCCTGATGATCCACAAGCCAG  
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGGAAACA  
GTACGATAATTATGGTGAAGAAGGATTAAGATGGTNATCAGAGCTCCCATGGAGACATTT  
TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA  
AATATTCCAAGAG

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**FIGURE 87**

GGCACGAGGCGGCGGGGCAGTCGCGGGATGCGCCCGGGAGCCACAGCCTGAGGCCCTCAGGT  
 CTCTGCAGGTGTCGTGGAGGAACCTAGCACCTGCCATCCTCTTCCCAATTTGCCACTTCCA  
 GCAGCTTTAGCCCATGAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**  
 AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTCTGGCTTCGTTTGACGCC  
 TTGGTGCTGGTTTGACAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATT  
 TAAGCCCATTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC  
 TGGACGATGTCGTTATCACCAACCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC  
 GAAGATGCCTCGGGTCTCATGTCCCCACTGCATTGCCATCTTGAAGATTGTACACTCTGAC  
 AGAGAAGCTTGTGGCATGACAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA  
 GCGACATCATTGTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG  
 TACCCTCCGTTGGACCCCAAACCTCCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTGAC  
 TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCTGGACTGGATTGACC  
 AGTCTCTGTGGCTGCTGAGGAGCATTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG  
 CCAGATAAAGGCCTCCAGGCCCTGAAGGCTTCTGCAGGAGCAGTCTGCAATT**TAGT**GCCT  
 ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCGCCCATCCCTGGATGGCTCAGCTTAGCCTT  
 CTACTTTTTCCATATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTAGCTGTGTGTGCATAG  
 TAAAGCAGGAGATCCCCGTCAGTTTATGCCTCTTTTGACAGTTGCAAACGTGGCTGGTGAGT  
 GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAA  
 CTGGTGGACTGTCAGCTTTATTTAGCTCACCTAGTGTTTTCAAGAAAATTGAGCCACCGTCT  
 AAGAAATCAAGAGGTTTCACATTAAATAGAAATTTCTGGCCTCTCTCGATCGGTCAGAATG  
 TGTGGCAATTCTGATCTGCATTTTCAGAAGAGGACAATCAATTGAAACTAAGTAGGGGTTTC  
 TTCTTTTGCAAGACTTGTACTCTCTCACCTGGCCTGTTTCATTTATTTGTATTATCTGCCT  
 GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGACAGTTTGGGTTTGAAGCTGAGGAAC  
 ACAAGTTGATGATTTCTTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG  
 GATAGTAAATTTATACTTATGTTTCCCTCAAAAAAAAAAAAAA

**FIGURE 88**

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSEL  
ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKTSA  
VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTALLSVSHLVLVTRNACHLTGGLDWI  
DQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI



**FIGURE 89**

GCTTCATTTCTCCCGACTCAGCTTCCACCCTGGGCTTTCGAGAGTGCTTTCGCCGCTGTCC  
CCACCACTGCAGCCATGATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA  
TTTGGAGTGTTTTCTGTTCTTTGGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT  
TGGAATGTTTTATTTGTAGCCGGCTTGGCTTTTGTAAATGGTTTAGAAAGAACATTGAGAT  
TCTTCTTCCAAAACATAAAATGAAAGCTACAGGTTTTTTCTGGGTGGTGTATTTGTAGTC  
CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTCTCTGTTTCAG  
GGGCTTCTTTCCTGTCGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT  
TTACCTGGAATTAGATCATTTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATTAACAACA  
AGTGAATTTGAAGACTCATTTAAAATATTGTGTTATTTATAAAGTCATTTGAAGAATATTCA  
GCACAAAATTAAATTACATGAAATAGCTTGTAAATGTTCTTTACAGGAGTTTAAAACGTATAG  
CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAACAGGCTTCTACTCAAGTGA  
ACTAAGAAGAAGTCAGCAAGCAAACAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA  
ACTCTTGAAGGCTATTTGTGTTGTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA  
CTGTGGTGCCTGTTTCTTTCTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT  
TTTTAGAAGTGTCCTGCAATGGCAAAAATATTCCAGTTGCACTGTATCTCTGGAAGTGA  
TGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTAACCAAGGAAACCCCAATTTTG  
ATGTATGGATTACTTTTTTTTGNCGNCAGGGCC

## **FIGURE 90**

MISLTDTQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQK  
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVLGSLNLPGI  
RSFVDKVGESNNMV

### **Important features:**

#### **Transmembrane domains:**

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

#### **N-myristoylation sites.**

amino acids 11-16, 51-56 and 116-121

#### **Aminoacyl-transfer RNA synthetases class-II protein.**

amino acids 49-59

**FIGURE 91**

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTTCTCCCGACTCAGCTTCCC  
ACCNTGGGCTTTCCGAGGTGCTTTTCGCCGCTGTCCCCACCACTGCAGCCATGATCTCCTTAA  
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTTGGAGTGTTTTCTCTGTTCTTGGA  
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTTGTAGCCGGCTT  
GGCTTTTGTAATTGGTTTAGAAAGAACATTCAGATTCTTCTTCCAAAAACATAAAATGAAAG  
CTACAGGTTTTTTCTGGGTGGTGTATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATG  
ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

**FIGURE 92**

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA  
GGCTGCCAGGAAGGAGACGCCTTCCTGAGTCTGGATCTTTCTTCTTCTGGAAATCTTTGA  
CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGGACCTCGCGGGACTGC  
TGAAGTCTCAGTTCCTGTGCCACCTGGTCTTCTGCTACGCTCTTATTGCCTCAGGGCTAATC  
ATCAACACCATTACGCTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCCGGAA  
GATCAACTGCAGACTGTCTTATGTCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT  
CGGGCACGGAATGCACCATCTTACGGACCCGCGCGCTACCTCAAGTATGGGAAGGAAAAT  
GCCATCGTGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA  
ACGCTTTGGGCTGTAGGGGGCTCCAAGGTCTGGCCAAGAAAGAGCTGGCCTATGTCCCAA  
TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTTCGCGCAAGTGGGAGCAGGAT  
CGCAAGACGGTTGCCACCAGTTTGCAGCACCTCCGGGACTACCCGAGAAGTATTTTTTCTCT  
GATTCACTGTGAGGGCACACGGTTTACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC  
GGGCCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC  
ACCGTGAGGAGCTTGAGAAATGTAGTTTCACTGTATATGACTGTACACTCAATTTCAGAAA  
TAATGAAAATCCAACACTGCTGGGAGTCTTAAACGGAAAGAAATACCATGCAGATTTGTATG  
TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGTCTCGGCTGGCTGCAC  
AAGCTCTACCAGGAGAAGGATGCCTTTCAAGGAGGAGTACTACAGGACGGGCACCTTCCAGA  
GACGCCCATGGTGCCCCCGGCGGCCCTGGACCTCGTGAAGTGGCTGTTTTGGGCCTCGC  
TGGTGCTCTACCTTTCTTCCAGTTCCCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACG  
CTGGCCAGCTTCATCTCGTCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT  
GACGGAATTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT  
GACTCAGGGAGGTGTCACCATCCGAAGGGAACCTTGGGGAAGTGGTGGCCTCTGCATATCCT  
CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCTGCTGGGCACGGCGGAAGTCACGA  
CCTCTCCAGCCAGGAGTCTGGTCTCAAGGCCGGATGGGGAGGAAGATGTTTTGTAATCTTT  
TTTTCCCATGTGCTTTAGTGGGCTTTGGTTTTCTTTTTGTGCGAGTGTGTGTGAGAATGGC  
TGTGTGGTGTGAGTGTGAACCTTTGTTCTGTGATCATAGAAAGGTATTTTAGGCTGCAGGGGAG  
GGCAGGGCTGGGGACCAAGGGGACAAGTTCCCCCTTTCATCCTTTGGTGTGAGTTTTCTGT  
AACCCTTGTTGCCAGAGATAAAGTGAAAAGTGCTTTAGGTGAGATGACTAAATTATGCCTC  
CAAGAAAAAAAATTAAGTGCTTTTCTGGGTCAAAAAAAAAA

**FIGURE 93**

MDLAGLLKSQFLCHLVFCYVFIA SGLIINTIQLFTLLLWPINKQLFRKINCRLSYCISSQLV  
MLEWWSGTECTIFTDPRAYLKYGKENAIVVLN HKFEIDFLCGWSLSERFGLLGSKVLAKK  
ELAYVPIIGWMWYFTMVFC SRKWEQDRKTVATSLQH LRDYPEKYFFLIHCEGTRFTEKKHE  
ISMQVARAKGLPRLKHHLLPRTKGFAITVRSLRNVVSAVYDCTLNFRNNENPTLLGVLNGKK  
YHADLYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQE EYYRTGTFPETPMVPPRRPWTLVN  
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRWMMIGVTEIDKGSAYGNSDS  
KQKLND

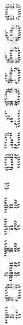
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**FIGURE 94**

CTGAGGCGGCGGTAGCATGGAGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCG  
 GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTCTTCTTGGGGAA  
 GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTA  
 TACAATTGACATTAGAAAATATATCCATGCTATCAGCTTTTTAGCTTTTATAATTCTTCAG  
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT  
 TGGTACAAATTCCGTCGTCATTGAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA  
 AAATTGACAGGAGCATTTTTCAAACCAAGACCTTGTTTTCTGCTATTAACACCAAGTATAA  
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCTTATATAAACCTCAAAAAGGACTT  
 TTTACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGTCTGAACAACCTGGGTTATAAAAC  
 TGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT  
 TTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA  
 CAAGAGGAATTAAGAGTATATGCAAAAAGTGGAAGACAGTGAACAAGCAGTAGATAAACT  
 AGTAAAGGATGTAACAGATTAAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTGAGG  
 CAGCAAGAGAGAAGAACATCCAAAAAGACCCTCAGGAGAACATTTTCTTTGTGAGGCATTA  
 CGGACCTTTTTTCCAAATTCTGAATTTCTTCATTATGTGTTATGTCTTTAAAAAATAGACA  
 TGTTTCTAAAAGTAGCTGTAACATAACCACCATCTCGATGTAGTAGACAATCTGACCTTAA  
 TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAGCAT  
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTAGATACACAAGA  
 CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC  
 CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCTACA  
 TTTTGAATCCTTTTAACCTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAGCCAAACAT  
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTTGTTTTTACTATGTTAC  
 CTGTTTGCAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAAC  
 ATCAGATGCTTTTATTTCCAAACCTTTTTTTCACCTTCTACTAAGTTGTTGAGGGGAAGGCT  
 TACACAGACACATTCCTTAGAATTGGAAGTGAGACCAGGCACAGTGGCTCACACCTGTAA  
 TCCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC  
 TGGGCAACGTATTGAGACCATGTCTATTAATAAATAAATGGAAGCAAGAATAGCCTTAT  
 TTTCAAATATGGAAGAAATTTATATGAAAATTTATCTGAGTCATTAAATTTCTCCTTAAG  
 TGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAATGCTGGATATCATGCA  
 ATAAATTTGCAAAACATCATCTAAATTTAAAAAAAAAAAAAAAAAAAAA

**FIGURE 95**

MEGESTSAVLSGFVLGALAFQHLNTDSDTGEFLLGEVKGEAKNSITDSQMDDVEVVYITIDIQ  
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEH  
FSNQDLVFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSC  
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN  
RLKREIEKRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSS  
CNYNHHLDVVDNLTLMVEHTDIPEASPASTPQIIKHKALDLDRAWQFKRSRLLDTDQKRSKA  
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTF



**FIGURE 96**

GGCACAGCCGCGCGCGGAGGGGAGAGTCAGCCGAGCCGAGTCAGCCGGACGAGCGGACGACGCGAGGCGAGC  
 CCAAGCAGCGCGCAGCGAACGCCCGCGCGCCACACCCCTCTGCGGTCGCCGCGGCGCTGCCACCCCTCCCT  
 CCTTCCC CGGTCGCCGCTCGCGGCCAGTCAGCTTGCCGGGTCGCTGCGCCGGAACCCCGAGGTCACCA  
 GCCCGCGCTCTGCTTCCCTGGGCGCGCGCGCTCCACGCCCTCCTTCTCCCTGGCCGCGCGCTGGCACC  
 GGGGACCGTGTGCTGACGCGAGGCCAGCTCTACTTTTCCGCCCGCGCTCTCCTCCGCGCTGCTGCGCTCTTCAC  
 CAACTCCAACTCCTTCTCCCTCCAGCTCCACTCGCTAGTCCCCGACTCCGCCAGCCCTCGGCCGCTGCCGTAG  
 CGCGCTTCCCGTCCGGTCCCAAAGGTGGGAACGCGTCCGCCCGCGCGCCACCA**Tag**GCACGGTTCCGCTTGCC  
 CGCGCTTCTCTGACCCCTGGCAGTGCTCAGCGCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGG  
 AAGTCGCGAGCTTTACGTGTCCAAAGGCTTCAACAAGAACGATGCCCCCTCCACGAGATCAACGGTGATCAT  
 TTGAAGATCTGCCCCAGGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAAGTAAAGA  
 TGATTTCAAAGGTGTGGTCAGCGAACAGTGCAATCATTTGCAAGCTGTCTTTGCTTCAGGTTACAAGAAGTTTG  
 ATGAATTTCTCAAAGAACTACTTGAATAATGCAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGGCCAT  
 TTATACATGCAAAATTTCTGAGCTATTTAAAGATCTCTTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGT  
 GAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCTCCTGGAGCGGATGTTCCGCCCTGGTGAACCTCCAGT  
 ACCACTTTACAGATGAGTATCTGGAATGTGTAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCCT  
 CGCAAAATGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCGTAAGTTTCGCTCAAGGCTTAGCGGTTGCGGG  
 AGATGTGCTGAGCAAGGTCTCCGTGGTAAACCCACAGCCAGTGTACCCATGCCCTGTTGAAGATGATCTACT  
 GCTCCCACTCGCGGGGTCTCGTGACTGTGAAGCCATGTTACAACACTACTGCTCAAACATCATGAGAGGCTGTTTG  
 GCCAACCAAGGGGATCTCGATTTTGAATGGAACAAATTCATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA  
 GGGTCCTTTCAACATTGAATCGGTATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGG  
 ATAATAGTGTTCAAGTGCTCAGAAGGTTTTCCAGGGATGTGGACCCCAAGCCCTCCAGCTGGACGAATT  
 TCTCGTTCATCTCTGAAAGTGCTTCAGTGCTCGCTTCAGACCACATACCCCGAGGAACGCCCAACCAACAGC  
 AGCTGGCACTAGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCCAAGAAATCTGTGCTCT  
 CCTTCCGAGCAACGTTTGCACGATGAGAGGATGGCTGCAGGAACCGCAATGAGGATGACTGTTGGAATGGG  
 AAAGGCAAAAGCAGGTACCTGTTTTCAGTGACAGGAATGGATTAGCCAACAGGGGCAACAACCCAGAGGTCGA  
 GGTTGACACCAGCAACACGACATACTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGA  
 AGAATGCATACAAATGGGAACGAGTGGACTTCTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGGAAAGT  
 GGCTGTGAGTATCAGCAGTGCCCTTCAGAGTTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAAATGA  
 GAAAGCCGACAGTGCTGCTGCTCGCTCTGGGGCACAGGCCTACCTCCTCACTGTCTTCTGCATCTTGTTCCTGG  
 TTATGCAGAGAGCTGGGAG**TAAT**TTCTCAAACCTCGAGAAAAAGTGTTTCATCAAAAAGTTAAAAGGCCACCACTT  
 ATCACTTTTCTACCATCCTAGTGACTTTGCTTTTAAATGAATGGACAACAAATGTACAGTTTTTACTATGTGGC  
 CACTGGTTTAAAGAAGTGCTGACTTTTGTCTTCTCATTCAGTTTTGGGAGGAAAAGGGACTGTGCATTTGAGTTGGT  
 TCCTGCTCCCCAAACCATGTTAAACGTGGCTAACAGTGTAGGTACAGAACTATAGTTAGTTGTGCATTGTGA  
 TTTTATCACTCTATTATTGTTTGTATGTTTCTTCTATTTCGTTTGTGGGTTTTTTTTTCAACTGTGATCT  
 CGCCTTGTCTTCTACAAGCAAAACAGGGTCCCTTCTTGGCACGTAACATGTACGTATTCTCGAAATATTAATA  
 GCTGTACAGAAGCAGGTTTATTATCATGTTATCTTATTAAAGAAAAAGCCCAAAAGC



**FIGURE 97**

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ  
GSTCCSQEMEKEYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF  
VKTYGHLYMQNSELFKDLFVELKRYVVGNNLEEMLNDFWARLLERMFRLVNSQYHFTDEY  
LECVSKYTEQLKPFQDVPRKLKLVTRAFVAARTFAQGLAVAGDVVSKVSVNPTAQCTHAL  
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLDFEWNNFIDAMLMVAERLEGPFNIES  
VMDPIDVKISDAIMNMQDNSVQVSQKVFQGCQPPKPLPAGRISRISSESASFARFRPHHPPEE  
RPTTAAGTSLDRLVTDVKEKLQAKKFWSSSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYLEF  
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGE  
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

**FIGURE 98**

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT  
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA  
GCAACTTACAGCTGCACCGACAGTTGCGATGAAGTTCTAATCTCTTCCCTCCTCCTGTTGC  
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCAC  
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA  
AGATTGGTTCTGAGAGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGC  
AGTGCCCCCTGTGATCATTTCAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGA  
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT  
TGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCTCCAATTAAACATTCTCAGCCAAGAA  
GACAGTGAGCACACCTACCAGACACTCTTCTTCTCCACCTCACTCTCCCACTGTACCCACC  
CCTAAATCATTCCAGTGCTCTCAAAAAGCATGTTTTCAAGATCATTTTGTTTGTTGCTCTC  
TCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTT  
AATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCTAGCTAGTGTCATTTAACCTTAAATGC  
AATCAGGAAAGTAGCAACAGAAAGTCAATAAATATTTTAAATGTCAAAAAAAAAAAAAAAAAA

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**FIGURE 99**

MKVLISSSLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR  
KFMTVSGLPKKQCPCDHFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

**FIGURE 100**

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCT  
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA  
AAGCCAGACTTCCCCAAATTCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA  
GTTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA  
AACATTTCATCAAAGTGACATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA  
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC  
TCCCAACGAGTTTCAGGATTTCAGGCTCTGGCTTCAACCAACAGAACTCATTTTGAACACC  
CTGACTGCATTTTGGCTTTTAGAAAGTTAGAATAAATATGGCGCTTGGGATCACATAGTTG  
ATGGAGAGGAAA

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**FIGURE 101**

MAVLVLRLTVVLGLLVFLTCYADDKPKDPDKPDDSGKDPKPDFPKFLLSLGTEIIEHAVE  
FILRSMSRSTGFMEFDDNEGKHSSK

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MAVLVLRLTVVLGLLVFLTCYADDKPKDPDKPDDSGKDPKPDFPKFLLSLGTEIIEHAVE  
FILRSMSRSTGFMEFDDNEGKHSSK

**FIGURE 102**

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT  
 CAGAGCTGGTCTGCC**ATG**GACATCCTGGTCCCACCTCCTGCAGCTGCTGGTGTCTTCTTAC  
 CCTGCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCTGTGCAAAAGCTACTTCC  
 CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG  
 CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGG  
 CTGCGGAACCGGAGCCAACCTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC  
 CAAATCCCCACTTTGAGAAGTTCTTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT  
 GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT  
 GGTGGTCTGCACTCTGGTGTGTGTCTGTGTCAGAGCCCAAGGAAGTCTGCAGGAGGTCC  
 GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTTCTGGGAGCATGTGGCAGAACCATATGGA  
 AGCTGGGCCCTTCATGTGGCAGCAAGTTTTTCGAGCCACCTGGAAACACATTGGGGATGGCTG  
 CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAATGG  
 AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC  
 AAACAATCTTTCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAACA  
 AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACC**TAG**CAGAATGAGAGAAGACATT  
 CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC  
 CCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC  
 TGTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTCCAATGTTGTC  
 CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGT  
 CTCTAGGAACTGGTCACAAAAGTCATGGTGCTGCATCCCTGCCAAGCCCCCTGACCTCT  
 CTCCCCACTACCACCTTCTTCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGGAT  
 GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTGTCTCAAATATTTTTTAATAAATAGACGA  
 AACCACG

**FIGURE 103**

MDILVPELLQLLVLLLLTLPLHLMALLGCWQPLCKSYFFPYLMAVLTPKSNRKMESKKRELFSQL  
KGLTGASGKVALLELGC GTGANFQFYPPGCRVTCLDENPHFEKFLTKSMAENRHLQYERFVV  
APGEDMRQLADGSMDVVVCTLVLC SVQSPRKVLQEVRRVLRPGGVLFWEHVAEPYGSWAFM  
WQQVF EPTWKHIGDCCLTRETWKDL ENAQFSEIQMERQPPPLKWL PVGPHIMGKAVKQSFP  
SSKALICSFPSLQLEQATHQPIYLP LRG T

TGTGGGATTTATTTTGAGTGCAAGATCGTTTTTCTCAGTGGTGGTGAAGTTGCCTCATCGCAG  
 CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA  
 ACTAATATTTATATGACAGAAGAAAAAG**ATGT**CATTCCGTAAAGTAAACATCATCATCTTGG  
 TCCTGGCTGTTGCTCTCTTCTTACTGTTTTGCACCATAAAGTTCCTCAGCTTGAGCAGTTTTG  
 TTAAGGAATGAGGTTACAGATTACAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCCAA  
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG  
 AAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTACAGCACAACTCGCTCCAAT  
 GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCCTGGCTCAACAG  
 TGATTCCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCTAACTTTTGAAGGAA  
 AAGTAAAGGAGGATCCTGACCAGGGGGAATCCATGAACCTTTAACCTTTGCAAGGTTCTAC  
 TTGCCAATTCTGTTTCCAGCGCAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA  
 AGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG  
 AAGATTGTGATTACGCCCTCTACTAAAGTTGTATCCGTGGAGCAGGAAACAGTACAATTAC  
 ATTGGCTATCTTGACTATAAAAAAGGAAAGAATTTCGTAAGCTTTCCATGAAAGCCAGCACTTG  
 CTCATTTAATCCTGGAGTTTTTTGTTGCAAACTGACGGAATGGAAACGACAGAATATAACTA  
 ACCAACTGGAAAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCTTGGCT  
 GGTAGCATCACAAACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC  
 TATGTGGAATGTCCGCCACCTTGTTTCCAGTGCTGGAAACGATATTACCTCAGTTTGTA  
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTGAAGCCATGGGGAAGGACTGCTTCATAT  
 ACTGATGTTTGGGAAAAATGGTATATTCAGACCCAAACAGGCAAAATTAACCTAATCCGAAG  
 ATATACCGAGATCTCAAACATAAG**TGA**AACAGAATTTGAAGTGAAGCAAGCATTCTCAG  
 GAAGTCCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA  
 GCAAGCCATGGAAAAAGATGTGTCAGCTAGGTAAGATGACAACTGCCCTGTCTGGCAGTC  
 AGCTTCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTTTTCTT  
 ACTACAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTTTACGCTAGCTGGTACAGA  
 TAATTCAAACTGCTGTTGGTTTTAATTTGTAACTGTGGCCTGATCTGTAAATAAACTT  
 ACATTTTTTC





**FIGURE 106**

TGGTTTTTGCCCCATAAATCCCTCAGCTTGAGCAGTTGTTAAGGAATGAGGTTACAGATT  
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT  
GGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT  
TGCAGCTATAAACAGCATTTCAGCACAACTCGNTCCAATGTGATTTTCTACATTGTTACTC  
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA  
TACAAAATTGTCAATTTTGACCCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA  
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCACAGCG  
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC  
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTAC  
TAAAGTTGTCATCCGTGGAGCAGGAAA

**FIGURE 107**

CGACGCTCTAGCGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG  
GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTGCAGGGAACGCGGGCGGCAGACAACGGGC  
TGGGCTCCGGGCGCTGCGGCGGGGCGCTGAGCTGGCAGGGCGGGTGGGGCGCGGGCTGCA  
TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGCCGCGGCGAGCCTTTGAGGGGAACGACT  
TGTGCGAGCCCTAACCAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGAGCGTCACATCACT  
TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT  
CCGTAAAGTAAACATCATCATCTTGGTCCTGGGCTGTTGCTCTCTTCTTACTGGTTTTGCAC  
CATAACTTCCTCAGCTTGAGGCAGTTTGTTAAGGAATGAGGTTACAGATTGAGGAATTGTAG  
GGCCTCAACCTATAGGACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA  
GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCGACTATAA  
ACAGCATTCAGCACAACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA  
GCAGACCATCTCCGGTCCTGGGCTCAACAGTGATTCCTGAAAAGCATCAGATACAAAATTG  
TCAATTTTGACCTTAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCC  
ATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGGTTCCGAGCGAAAGAAGG  
CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCA  
CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTACTAAAGTTGT  
CATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATAAAAGGAAAGAA  
TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAC  
CTGACGGAATGGAACGACAGAATATAACTAACCACTGGAAAAATGGATGAACTCAATGT  
AGAAGAGGGACTGTATAGCAGAACCTGGCTGGTAGCATCACAAACCTCCTCTGCTTATCG  
TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGT  
GCTGGAAAACGATATTACCTCAGTTTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACA  
TTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGGAAAAATGGTATATPCCA  
GACCCAACAGGCAAATTCACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAAA  
CAGAATTTGAACTGTAAGCAAGCATTTCTCAGGAAGTCTGGAAGATAGCATGCGTGGGAAG  
TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTGAGCTAG  
GTAAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCGAGACAGACTATAGACTATAAAT  
ATGCTCCATCTGCCTTACCAAGTGTCTTCTTACTACAATGCTGAATGACTGGAAAGAAGAA  
CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAACTGCTGTTGGTTTTAATTTT  
GTAACCTGTGGCTGATCTGTAAATAAACTTACATTTTTCAATAGGTAAAAAAAAAAAAA  
AAAAAA

**FIGURE 108**

CTGCAGGTAGACATCTCCACTGCCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT  
GAAGGCCGGCCATACCAGAGTCTCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG  
TCTGTGCTGGTCTGAGGGTGTGCTGCTGTC**ATG**GGGGCAGCCATCTCCAGGGGGCCCTCATC  
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTCTGGGTCTCCTCTGCTG  
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC  
TGGCCCCTGTCTGAGAAGGCCCCACCACCCAGAAAGCCAGCCATGAAGGCAGCTACCTGC  
TGCAGCCCTGAAGGCCCCTGGCCTAGCCTGGAGCCCAGGACCT**TAA**GTCCACCTCACCTAGAG  
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT  
TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC  
TAAGGAGATGGGCCTGGGGTGGGGGCTTATGAGTTGGTGCTAGAGCCAGGGCCATCTGGACT  
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTTCCCTAGGCTGAGCACC  
TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCCAG  
GCTGGGCCCTCCCTGGTCTCCAGTGTTTGCTGGATAATAAATGGAACCTATGGCTCTAA  
AAAAAAAAAAAAAAAA

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**FIGURE 109**

MGAAISQGALIAIVCNGLVGFLLLLLWVILCWACHSRLPTLTLSLNPVPTPALAPVLRPHH  
PRSPAMKAATCCSPEGFWPSLEPRT

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MGAAISQGALIAIVCNGLVGFLLLLLWVILCWACHSRLPTLTLSLNPVPTPALAPVLRPHH  
PRSPAMKAATCCSPEGFWPSLEPRT

GTTTGAATTCCTTCAACTATATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCA  
 GTTCCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA  
 CTCCTTATTTGCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTTCTAAGTGGAA  
 TC**ATG**TGCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGCTCTTTGGCC  
 ATGATGTTTTACCTTCAGATTTCATCACCACCCTTCTGGTTCACATTTTCATTTTCATTGGTTAT  
 TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC  
 TCAGCATAGAATTGGACACAGAAGGGGAAAATATGAAGTGCCTGCTGGGGTTTGCTATCGTA  
 TCCACAGGCATCACGGCAGTGCTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATT  
 GACAGTTGAGCTTTTCCAAATCACAAATAAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCC  
 AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTG  
 AGCCTGGGAACTGCAGGAGCTGCCAGGTTATGGAAGGCGGCCAAGTGAATATAAGCCCCCT  
 TTCGGGCATTCGGTACATGTGGTCGTACCATTTAATTGGCCTCATCTGGACTAGTGAATTC  
 TCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAGTGGTACTTGTTATTTCAACAGAAGT  
 AAAAATGATCCTCCTGATCATCCCATCCTTTCTGCTCTCTCCATTCTCTTCTTCTACCATCA  
 AGGAACCGTGTGTAAAGGGTCATTTTTAATCTCTGTGGTGAGGATTCGAGAAATCATTTGTCA  
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA  
 TGCTGCTACTGCTGTTTCTGGTGCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA  
 TACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAAATCT  
 TGTCCAAGAACTCAAGTCACTTTACATCTATTAAGTGCCTTTGGAGACTTCATAATTTTTCTA  
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACACAAATCG  
 GGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTTGGCTACTTAGTAGCCC  
 ATAGTTTTTTATCTGTGTTTGAACCTGTGCTGGATGCACTTTTCTGTGTTTTGCTGTTGAT  
 CTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT  
 CGTAAAAAGGAGCAACAAATTAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGA  
 ATGAGGAGGGAACAGAACTCCAGGCCATTGTGAGAT**TAG**ATACCCATTAGGTATCTGTACCT  
 GGAAAAATTTCTTCTTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTT  
 AGTGAATTTTTTTTTAAAGACCTAATAAACCCCTATTCTTCTCTCAAAA

**FIGURE 111**

MSGRDTILGLCILALALSLAMMFTFRFITTLVHIFISLVILGLLFVCGVLWWLYDYDNDL  
SIELDTERENMKCVLGFIAIVSTGITAVLLVLIFVLKRRIKLTVELFQITNKAISSAPFLFQ  
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI  
LACQQMTIAGAVVTCYFNRSKNDDPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVM  
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKIL  
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAH  
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN  
EEGTELQAIVR

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MSGRDTILGLCILALALSLAMMFTFRFITTLVHIFISLVILGLLFVCGVLWWLYDYDNDL  
SIELDTERENMKCVLGFIAIVSTGITAVLLVLIFVLKRRIKLTVELFQITNKAISSAPFLFQ  
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI  
LACQQMTIAGAVVTCYFNRSKNDDPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVM  
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKIL  
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAH  
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN  
EEGTELQAIVR

[illegible]



**FIGURE 113**

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINC DVKAGKIIDPEFIVKC  
PAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSL  
SLPRWRESFIVLESKPKKGVITYPSALTYSSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQ  
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTTSSQNRPRADPGIQ  
RQDPGSAAFQKPGVADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFR  
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAIEKITQRGGLSNV  
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAEE  
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLOPLVKRVCDTDRLACSKTCLNSADI  
GFVIDGSSSVGTGNFRTLQFVTNLTKEFEISDTDTRIGAVQYTYEQRLEFGFDKYSSKPDII  
LNAIKRVGYWSGGTSTGAAINFALEQLFKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG  
VITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRIIQNICTEFNSQPRN

CAGGATGAACGTGGTTGCAGTGGCTGCTGCTGCTGCGGGGCGCTGAGAGGACACGAGCTCTA**TG**CCCTTTCCGGCTGCTCATCCCGCTCGGCCCTCTGTGCGCGCTGCTGCCTCAGCACCATTGGT  
GCGCCAGGTCCCAGCGCTCCGCGCCAGATCCCGCCCACTACAGTTTTTCTCTGACTCTAAT  
TGATGCACGTGGACACCTTGTGATTTTGGGGAATGTCTCAGAATTCCAAGAGTGGTTGAAG  
TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCTCTGTGTTTGAACAAACATT  
CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGTGGAAGTAGA  
GGCTGGATGGCCCTGTTCCGGGCCTCTCCTGAGAATGGCTGAGGAGCGGCCCGAAACTCC  
TCCAGCCTTTAGACCCCCACTGGCATGCCATATGGAACAGTGAACCTACTTCATGGCGTG  
AACCCAGGAGAGACCCCTGTCACTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC  
CACCTTGAGCAGCCTCACTGGTGACCCGGTGTTCGAAGATGTGGCCAGAGTGGCTTTGATGC  
GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCACATTGATGTGCTCACTGGC  
AAGTGGGTGGCCAGGACGCAAGGCATCGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGT  
GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTTAGAGTATAACAAAG  
CCATCCGGAACCTACACCCGCTTCGATGACTGGTACCTGTGGGTTTCAGATGTACAAGGGGACT  
GTGTCCATGCCAGTCTTCCAGTCTTGGAGGCCACTGGCCTGGTCTTCAGAGCCTCATTTGG  
AGACATTGACAATGCCATGAGGACCTTCTCAACTACTACACTGTATGGAAGCAGTTTGGGG  
GGCTCCCGGAATTCTACAACATTCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA  
CTTCGGCCAGAACCTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCACCCT  
CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTGC GGAT  
TTGCAACAATCAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCTCTG  
GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCAACTTCATCCACAACATGG  
GTCCACCTTCGACGCGGTGATACCCCCCTATGGGGAGTGCATCTGGGGGCTGGGGGGTACA  
TCTTCAACACAGAAGCTCACCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG  
GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGTC  
GAAATTTAGAAAAACACTGTTAGTTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC  
TCTTCTACCCAGAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAAGTCCCA  
CTTCTCAGCTGCCCCAGTCAGCCCTTCACCTCCAAGTTGGCATTACTGGGACAGGTTTTCTCT  
AGACTCCTCATA**TA**ACCACTGGATAATTTTTTTATTTTTATTTTTTTGAGGCTAACTATAATA  
AATTGCTTTTGGCTATCATAAAA

**FIGURE 115**

MPFRLLIPLGLLCALLPQHGHGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE  
VLQDSVDFDIDVNASVFETNIRVVGLLSAHLLSKKAGVEVEAGWPCSGPLLMAEEAARKL  
LPAFQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM  
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK  
AIRNYTRFDDWYLVWQMYKGTVSMVPVFSLEAYWPGLQSLIGDIDNAMRTFLNYYTVWKQFG  
GLPEFYNIQQGYTVEKREGYPLRPELIESAMYLYRATGDPTLLELGRDAVESIEKISKVECG  
FATIKDLRDHKLDRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGY  
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGWPWEPPARPGT  
LFSPENHDQARERKPAKQKVPLLSCPSQPFTSKLALLGQVFLDSS

**FIGURE 116**

AAAGTTACATTTTCTCTGGAACCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG  
 GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA  
 ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT  
 GAGATGGACAGAATGCTTTATTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA  
ATGCCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT  
 ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC  
 TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTGATCGCGCCTGGAGA  
 AACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT  
 GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTGATGTCACTGATGACATC  
 ACGGCCACTGTGCCATAACAACCTTCGTGTGTCAGGGCCACATTGGGCTCAGACCTCAGCCTG  
 GAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA  
 TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC  
 CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG  
 GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACCTGTGTGAAGGCCAGA  
 CATTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA  
 GGAGAGGCCATTCCCCTGGTACTGGCCCTGTTTGCCCTTGTGGCTTCATGCTGATCCTTGT  
 GGTCTGCCACTGTTTCGTCTGAAAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGTGG  
 TGGTCTCCAGACACCTTGAAAATAACCAATTACCCAGAGTTAATCAGCTGCAGAAGG  
 GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCAGGGCCTGGAT  
 CTCATAGTTTTGCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACC  
 ATGAGGGGACAAGTTGTGTTTCTGTTTTCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA  
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC  
 TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGCTGCCACTTGCTGGCTGAGCAACC  
 CTGGGAAAAGTGACTTCATCCCTTCGGTCCTAAGTTTTCTCATCTGTAATGGGGGAATTACC  
 TACACACCTGCTAAACACACACACAGAGTCTCTCTCTATATATACACAGTACACATAAA  
 TACACCCAGCACTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTAG  
 TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT  
 GGCTTGGAGAGCCACTTTCCAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG  
 TGTTGAGTTCACTTCAAGCCCAATGCCGGTGAGAGGGGAATGGCTTAGCGAGCTCTACAGT  
 AGGTGACCTGGAGGAAGGTCACAGCCACACTGAAAAATGGGATGTGCATGAACACGGAGGATC  
 CATGAACACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT  
 GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC  
 TGTTGGTAAAGTACAGAATTCAGCAAATAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA  
 AAAAAAAAAA

**FIGURE 117**

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAIGE  
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECVTDITATVPYNLRVRATLGSQTS  
SILKHPFNRNSTILTRPGMEITKDGFLVIELEDLGPQFEFLVAYWRREPGEAEHVKMVRSG  
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPVLALFAFVGFMILV  
VVPFLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

**Important features:****Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 230-255

**N-glycosylation sites.**

amino acids 40-43 and 134-137

**Tissue factor proteins homology.**

amino acids 92-119

**Integrins alpha chain protein homology.**

amino acids 232-262

**FIGURE 118**

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT  
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA  
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG  
TCAAAGTGAAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT  
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC  
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA  
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGCGAATACCAGGGGGAGTACGAGAGCCT  
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGTCTCTGAGTGTG  
ATGTCACTGATGACATCACGCCACTGTGCCATACAACCTTTGTGTGAGGGCCACATTGGGC  
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC  
CCGACCTGGGATGGAGATCACCAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG  
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG  
GTTNCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC  
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

**FIGURE 119**

CGGACGCGTGGGCCGCCACCTCCGGAACAAGCCATGGTGGCGGCGACGGTGGCAGCGGCGTG  
GCTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGG  
TCAACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGCGGATCCGTGTCCCTGGTGGTG  
AATGTGGCCAGCGAGTGCGGGCTTACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG  
AGACCTGGGCCCCACCACTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGGCCAACAGG  
AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCCGCCGACCTACAGTGTCTCATTTCCC  
ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCTGCCTTCAAGTACCTGGCCCCA  
GACTTCTGGAAGGAGCCCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAGG  
TGGTAGGGGCTTGGGACCCAACTGTGTGCTAGTGGAGGAGTTCAGACCCAGATCACAGCGCTC  
GTGAGGAAGCTCATCTACTGAAGCGAGAAGACTTATAACCACCGCGTCTCCTCCTCCACCA  
CCTCATCCCGCCACCTGTGTGGGGCTGACCAATGCAAACTCAAATGGTGCTTCAAAGGGAG  
AGACCCACTGACTCTCCTTCTTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAA  
AAATTCTAGTATTTTGATTATTTGAATCTTACAGCAACAAATAGGAACTCCTGGCCAATGAG  
AGCTCTTGACCAGTGAATCACCAGCCGATACGAACGTCTTGCCAACAAAAATGTGTGGCAAA  
TAGAAGTATATCAAGCAATAATCTCCCACCAAGGCTTCTGTAAACTGGGACCAATGATTAC  
CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC  
CAAATAGGAGGCATTCAATGAACATTTTTTGCATATAAAACCAAAAAATAACTTGTTATCAAT  
AAAAACTTGCATCCAAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT  
GTTATTTCTCTGTATTATTTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCA  
AACAAATACCTCACGATATAAAATAAAAAATGAAAGTATCCTCCTCAAAAA

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**FIGURE 120**

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLEKYRGSVSLVNVASECGFTDQ  
HYRALQQQLQRDLGPHHFNVLAFFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG  
AHPAFKYLAQTSGKEPTWNFWKYLVPDGGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

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**FIGURE 121**

CGGACGCGTGGGCGGGCCGGGACGCAAGCGAGGCC**ATGG**GCTGTCTACGTCGGGATGC  
 TGCGCCTGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGTCTGGGGGCCCGGCCGCCCTCTCT  
 CGGAGTTGGCAGGAAGCCAGGTTGCAGGGTGTCCCGTTCCTCAGTTCCAGAGAGGTGGATCG  
 CATGGTCTCCACGCCCATCGAGGCCCTCAGCTACGTTCAAGGGTGCACCAAAAGCATCTTA  
 ACAGCAAGACTGTGGGCCAGTGCCTGGAGACCACAGCACAGAGGGTCCCAGAAGCAGAGGCC  
 TTGGTCGTCTCCATGAAGACGTAGGTTGACCTTTGCCAACTCAAGGAGGAGGTGGACAA  
 AGCTGCTTCGGCCTCCTGAGCATTGGCCTCTGCAAAGGTGACCGGCTGGGCATGTGGGGAC  
 CTAACCTCTATGCATGGGTGCTCATGCAGTTGGCCACCGCCAGGCGGGCATCATTCTGGTG  
 TCTGTGAACCCAGCCTACCAGGCTATGGAACGAGGATATGCTCTCAAGAGGTGGGCTGCAA  
 GGCCCTTGTGTCCCCAAGCAATTCAAGACCAGCAATACTACAACGTCCTGAAGCAGATCT  
 GTCCAGAAGTGGAGAATGCCAGGCCAGGGGCCCTGAAGAGTCAGAGGCTCCAGATCTGACC  
 ACAGTCATCTCGGTGGATGCCCTTTGCCGGGGACCTGTCTCTGGATGAAGTGGTGGCGGC  
 TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATACAACAGCAGTTCCTGTCTGCCATG  
 ACCCATCAACATCCAGTTACCTTCGGGACAACAGGCAGCCCCAAGGGGGCCACCCTCTCC  
 CACTACAACATTGTCAACAACCTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGAC  
 ACCAGAGCAGTTGCGGATGATCCTGCCCAACCCCTGTACCATTGCCTGGGTTCCGTGGCAG  
 GCACAATGATGTGTCTGATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGC  
 AAGAAGGCACTGGAGGCCATCAGCAGAGAGAGAGGCCACCTTCCTGTATGGTACCCCCACGAT  
 GTTCGTGGACATTCTGAACAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAG  
 GTGTCAATTGCTGGGTCCCCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAT  
 ATGAAGGACCTGGTGGTTGCTTATGGAACACAGAGAACAGTCCCGTGACATTGCGCGCACTT  
 CCCTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGG  
 CCCGGATCATGAACATGGAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGC  
 ATCCAGGGTACTGCGTCATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGT  
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTGCGCCACAATGAATGAGCAGGGCTTCTGCA  
 AGATCGTGGGCGCTCTAAGGATATGATCATCGGGGTGGTGAGAATCTACCCCGCAGAG  
 CTCGAGGACTTCTTTCACACACACCCGAAGGTGCAGGAAGTGCAGGTGGTGGGAGTGAAGGA  
 CGATCGGATGGGGGAAGAGATTTGTGCTGCAATTCGGCTGAAGGACGGGAGGAGACCACGG  
 TGGAGGAGATAAAAGCTTTCTGCAAAGGGAAGATCTCTCACTTCAAGATTCCGAAGTACATC  
 GTGTTTGTCAAACTACCCCTCACCATTTCAGGAAAGATCCAGAAATTCAACTTCGAGA  
 GCAGATGGAACGACATCTAAATCTG**TGA**ATAAAGCAGCAGGCCTGTCTGGCCGGTTGGCTT  
 GACTCTCTCCTGTGCAATGCAACCTGGCTTTATGCACCTAGATGTCCCAGCAGCCAGTTT  
 TGAGCCAGGCACATCAAAATGTCAAGGAATTGACTGAACGAATAAGAGCTCCTGGATGGGTC  
 CGGGAACCTCGCTGGGCACAAGGTGCCAAAAGGCAGGCAGCTGCCAGGCCCTCCCTCTG  
 TCCATCCCCCACATTCCTGTCTGTCTTGTGATTGGCATAAAGAGCTTCTGTTTTCTTT  
 GAAAAAAAAAAAAAAAAA

**FIGURE 122**

MAVYVGMLRLGRLCAGSSGVLGARAALSRSWQEARLQGVRFLSSREVD RMVSTPIGGLSYVQ  
GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG  
DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY  
YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLPGTLLLEVVAAAGSTRQHLDQLQYN  
QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY  
HCLGSVAGTMCMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY  
DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENSPTFAHFPEDTVEQKAESVG  
RIMPHTEARIMMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKWYWTGDVAT  
MNEQGFCIKIVGRSKDMIIRGENIYPAELEDFHTHPKVQEVQVGVKDDRMGEEICACIRL  
KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

**Signal Peptide:**

amino acids 1-22

**Transmembrane Domains:**

amino acids 140-161, 213-229, 312-334

**Putative AMP-binding Domain Signature:**

amino acids 260-271

**N-myristoylation Sites:**

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,  
314-319, 318-323, 379-384, 380-385, 409-413

**N-glycosylation Site:**

amino acids 282-285

**FIGURE 123**

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA  
TGATCCTGCCCAACCCCTGTACCATTGCCTGGGTTCCTGGCAGGCACAATGATGTGTCTG  
ATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACTGGAGGC  
CATCAGCAGAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGATGTTCTGGACATTCTGA  
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC  
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT  
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTTCCCTGAGGACACTGTGG  
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG  
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCCGGGAGCTGTGCATCCGAGGGTACTGCGT  
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT  
ATTGGACAGGAGATGTCGCCAC

**FIGURE 124**

GAGCAGGACGGAGCC**ATG**GACCCCGCCAGGAAAGCAGGTGCCAGGCCATGATCTGGACTGC  
 AGGCTGGCTGCTGCTGCTGCTTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG  
 TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCCGCGCCGGC  
 GTGGACGTCTGCACCGAGGCCGTGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC  
 AGTGCGGGGTTCGGTTTCGGGACTCCCCGGCAAGAATGACCGCGCCTGGATCTTCACGGC  
 TTCTGGCGTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC  
 ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCCGCCAACGGCGTGGAGTG  
 CTACAGCTGTGTGGGCCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGGTTCGTGAGCT  
 GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTCACCTTGACGGCA  
 GCTAATGTGACTGTGTCTTTCCTGTCCGGGCTGTGTCCAGGATGAATTCTGCACTCGGGA  
 TGGAGTAACAGGCCCAGGGTTACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAACCT  
 CTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATCCACCCCTTGTCCGGCTGCCCCCT  
 CCAGAGCCCACGACTGTGGCCTCAACCACATCTGTCAACCTTCTACCTCGGCCCCAGTGAG  
 ACCCACATCCACCACCAAAACCCATGCCAGCGCCAACCAAGTCAGACTCCGAGACAGGGAGTAG  
 AACACGAGGCCTCCCGGGATGAGGAGCCCAGGTTGACTGGAGGCGCCGCTGGCCACCAGGAC  
 CGCAGCAATTCAGGGCAGTATCCTGCAAAAGGGGGCCCCAGCAGCCCCATAATAAAGGCTG  
 TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTGT**G**  
**G**AGCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT  
 CATCACTTCTGTTCCCACTGACTGGGCTGGCCAGCCCTGTTTTTCCAACATTCCC  
 CAGTATCCCAGCTTCTGCTGCGCTGGTTTTCGGCTTTGGGAAATAAAATACCGTTGTATAT  
 ATTCTGCCAGGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTC  
 TCCGCTTGTCTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTCACGGGGAAGGTG  
 AGAGAGAGGATGCTAAGCTTCTACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGG  
 GGTGGTGGGACAATGGCTCCCACTCTAAGCACTGCCTCCCTACTCCCGCATCTTTGGG  
 GAATCGGTTCCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGCCCCGGTAC  
 CCAATTCGCCCTATAGTGAGTCGTA

**FIGURE 125**

MDPARKAGAQAAMIWTAGWLLLLLLLRGGAQALECYSCVQKADDGCSPNKMKTVKCAPGVDVCT  
EAVGAVETIHGQFSLAVRGCGSGLPGKNDRGLDLHGLLAFIQLQQCAQDRCNAKLNLTSRAL  
DPAGNESAYPPNGVECYSCVGLSREACQGTSPVVCYNASDHVYKGCDFGNVTLTAA NVTV  
SLPVRGCVQDEFCTR DGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRIPLVRLPPPEPTT  
VASTTSVTTSTSAFVRPTSTTKMPAPTSTQTPRQVEHEASRDEEPRLTGGAAGHQDRSNG  
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

[illegible]

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**FIGURE 127**

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK  
CSFNQKPRAPGDEEAQVENLITANATEPQKQRTVEQPSGGSLWNLRRLLEPLDANVDA

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

**FIGURE 128**

AAACTTGACGCCATGAAGATCCCGGTCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT  
CCACTCTGCCCAGGGAGCCACCCTGGGTGGTCTGAGGAAGAAAGCACCATTGAGAATTATG  
CGTCACGACCCGAGGCCTTTAACACCCCGTTCTGAACATCGACAAATTGCGATCTGCGTTT  
AAGGCTGATGAGTTCTTGAAGTGGCAGCCCTCTTTGAGTCTATCAAAGGAAACTTCCTTT  
CCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAGT  
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT  
CTTTCCTGCCTCAGGAACCTCAATAAAACATTTTCCATCCAAA



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**FIGURE 129**

MKIPVLPVAVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKADE  
FLNWHALFESI KRKL PFLNWDAFPKLGKLSATPDAQ

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MKIPVLPVAVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKADE  
FLNWHALFESI KRKL PFLNWDAFPKLGKLSATPDAQ

**FIGURE 130**

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC  
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTC  
TTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC  
TTTGCCGGCCACTCATGAGAGTGTTTTTGTGTAAAGTATTTTTAGAACTACTGTTGACTTCT  
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCTCA  
AATTTTGTATTACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCCTTTATTTTT  
AGGTTCAAGGTTCAATTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTATTATC  
TTCATTATTAATTGTAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTT  
TATCCCTGGGTGCCCCTGACACATTTATGTAGTGATCCACAAATGTGATIGTTAATTTAAA  
TGTTATTCTAATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT  
AAAAGTTTGTAGTATATTTTTCAACTAGATATTGTATAGAAAGACTGAATAGTGATG

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**FIGURE 131**

MGVEIAFASVILTCLSLAAGVSQVLLQPVPTQETGPKAMGDLSCGFAGHS

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MGVEIAFASVILTCLSLAAGVSQVLLQPVPTQETGPKAMGDLSCGFAGHS

**FIGURE 132**

GGGGAATCTGCAGTAGGTCTGCCGCG**ATG**GAGTGGTGGGTAGCTCGCCGCTTCGGCTCTG  
 GCTGCTGTTGTTCTCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAATGGA  
 AAGTATTTATTGACCAAATTAACAGGTCTTTGGAGAATTACGAACCATGTTCAAGTCAAAAC  
 TGCAGCTGCTACCATGGTGT CATAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG  
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA  
 GACTGTACCCGGGAAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTATT  
 TTGGAAGTGATCGGGCGTCTCCCTGCATGGAGATGGTGATCAATGTACGAGATTATCCTCA  
 GGTTCCTAAATGGATGGAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC  
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGACCTGCTGTTTGGCCAATTTAT  
 CCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTGACGACGACAGTG  
 GCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG  
 ATCTCTCATTTCTTCTGTCTCGGAAAAACCCAAAACCTTGTGTGATGCAGAATACACCAAAAAC  
 CAGGCCTGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT  
 GGATCACTGCAAAATACAAGTATCTGTTTAAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA  
 AACACCTCTTCTGTGTGGCTCACTTGTTTTCCATGTTGGTGATGAGTGGCTAGAATTCTTC  
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCCAGTCAAAACAGATCTCTCCAATGTCCA  
 AGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA  
 GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG  
 AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAT  
 TCCCAAAATGTTGAAAAC**TGA**ACTAT**AG**TAGTCATCATAGGACCATAGTCTCTTTGTGGCA  
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA  
 TCTGCTATCAAGCCAAATACCTGGTTTTCCTTATCATGCTGCACCCAGAGCAACTCTTGAGA  
 AAGATTTAAATGTGTCTAATACTGATATGAAGCAGTTCACTTTTGGATGAATAAGGA  
 CCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTCAATTTCTTAAGACCAATC  
 ACAGCTTGTGCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA  
 TGTGATGATGCCCTTTGTCCCATTATTTGGAGCAGAAAATTCGTCATTTGGAAGTAGTACAA  
 CTCATTGCTGGAATTGTGAAATTATTCAAGGCGTGATCTCTGTCACTTTATTTTAAATGTAGG  
 AAACCCATATGGGTTTATGAAAAATACTTGGGGATCATTCTCTGAATGGTCTAAGGAAGCGG  
 TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTGTAAAACCATAAACTCTGTTACTCAG  
 GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATT  
 TCAGGTTCCCTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

**FIGURE 133**

MEWWASSPLRLWLLLFLLPSAQGRQKESGSKWKVFIDQINRSLENYEPCSSQNCSCYHGVE  
EDLTPFRGGISRKMMAEVVRRKLGTHYQITKNRLYREND CMFPSRCSGVEHFILEVIGRLPD  
MEMVINVRDYPQVPKWMEPAIPVFSFSKTSEYHDIMYPAWTFWEGGPAVWPIYPTGLGRWDL  
FREDLVRSAAQWPWKKKNSTAYFRGSRTSPERDPLILLSRKNPKLVDAEYTKNQAWKSMKDT  
LGKPAAKDVHLVDHCKYKYLNFNRGVAASFRFKHLFLCGSLVFHVGDWLEFFYPQLKPWVH  
YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMDDITCYWENLLSEYSKFLSY  
NVTRRKG YDQII PKMLKTEL

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**FIGURE 134**

CACCCCTCCATTTCTCGCC**ATG**GCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT  
TCATCCTGGCCTTTGGCACCGGAGTGGAGTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT  
GGAGGGATCCCGGAGTCTGGTGGTCCGGATGCCCCCAGGGATGGCTGGCTGCCCTGCAGGA  
CCGAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTTGTTGGGCAGC  
ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCCTTCAG  
AGGTCACGTATGTGGCCTGCACTGCCCTGGCCTTGCACTGGTGATGCGGTACTGGGAGCC  
CATACCCAAAGGCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCGC  
TCCTCTGCTTTGTGCTCCATGTCTCTCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT  
GACTATGCTGAGCTCATGGGCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC  
TCTGGCCCTGAAGTCTCCCGGGCTCTCAGACTCTTCTCCACCTGCGCCACCCAGTGTGTG  
TGGAGCTGCTGACAGTGTGTGGGTGGTGCCTACCTGGGCACGGACCGTCTCCTCCTTGCT  
TTCTCCTTACCTCTACCTGGGCCTGGCTCAGGGCTTGATCAGCAAGACCTCCGCTACCT  
CCGGGCCCAGCTACAAAGAAAACCTCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAG**T**  
**G**AGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCTCCCACTGAATTCTAAATCCTTAAC  
ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCTT  
CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCCTAAATTCTGAGTTTCAGCCA  
CTGAACTCCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC  
TTCAGTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC  
CTGACCACTCCCCTGGCACGTACTTGCCTCTGCGCCTCAGGGTCCCCCTTCTGCACCGCT  
GGCTTCCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTCAACGGTCATAGCTGTCCCTCCA  
GGCCCCAACCTTGCTCACCCTCCCGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT  
GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAACTCGATGACTTGGGGCTC  
CTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAGTCAGCCTTTTTCTAAAAAAA

**FIGURE 135**

MAPALLLI PAALASFILAFGTGVEFVRFTSLRPLLGGIPESGGPDARQGWLAALQDRSILAP  
LAWDLGLLLLLFVGQHSLMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV  
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAELMGLKQVYHVVLGLGEPLALKSP  
RALRLFSHLRHPVCVELLTVLWVPTLGTDRLLLAFLTLYLGLAHGLDQQDLRYLRAQLQR  
KLHLLSRPQDGEAE

**Signal sequence:**

amino acids 1-13

**Transmembrane domains:**

amino acids 58-76, 99-113, 141-159, 203-222

**N-myristoylation sites:**

amino acids 37-43, 42-48, 229-235

**FIGURE 136**

CCGAGCAGCAGGAGATTGCCCTGCGTTTATAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA  
AGAAATTGCCAAACCATGTCCTTTTTTCTGTTTTTCAGAGTAGTTCCACAACAGATCTGAGTGT  
TTTAATTAAGCATGGAATACAGAAAAACAACAAAAAACTTAAGCTTTAATTTTCATCTGGAATT  
CCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA  
TCACGTGGTGCTCTCCGACTACTCACCCCGAGTGTAAGAACCCTTCGGCTCGCGTGCTTCTG  
AGCTGCTGTGGATGCGCTCGGCTCTCTGGACTGTCCTTCCGAGTAGGATGTCACTGAGATCC  
CTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTTGATGTGGTACCTCAGCCCT  
TCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTT  
ACAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAATCCATTT  
CTGGTCATTCTGGTGACCTCCCACCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC  
TTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAG  
AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCTTAGAGGATGAACACCTTCTTTATGGT  
GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTATGGC  
ATTCAGGTGGGTAACAGAGTTTTTGCCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG  
TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTT  
TTCACAGTTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAAACCATAT  
TCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTTGGGTTATATAA  
TGTCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTACGTAAAACCCATCAAGTTT  
GAAGATGTTTATGTGGGATCTGTTTGAATTTATTAAAGTGAACATTCATATCCAGAAGA  
CACAAATCTTTTCTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG  
CAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTTGGCAGGTCATGCTAAGGAACACC  
ACATGCCATTATTAACCTTCACATTCTACAAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA  
GTGTTAAATAAAGTAGGTACTGTGGAAAATTTCATGGGAGGTCACTGTGCTGGCTTCACTG  
AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTCACTTGTGATTATTAGTC  
AGGCCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTTGCTAAA  
GAAATTAATAGGACCAACAATTTGGACATGTCTATTCTGTAGACTAGAATTTCTTAAAGGG  
TGTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAAACAATGTAGAGTTTTATTATTATG  
AACAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGATTACCAATTTAAAAATATA  
TGTAGTTCTGTGTCAAAAAACTTCTTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTT  
TGCTCATTTTATAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTAAATTA  
CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAAT  
CATTTCTTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC  
TCCATTAATGTAAAGTCATAGGTCAATTATGCATATCAGTAATCTCTTGGACTTTGTTAAAT  
ATTTTACTGTGGTAAATATAGAGAAGAATTAAAGCAAGAAAATCTGAAAA



**FIGURE 137**

MASALWTVLPSRMSLRSLKWSLLLLLSLSSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQD  
FHFTLREHSNCSSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EK  
EDKMLALSLEDEHLLYGDIIRQDFLDTYNNLT LKTIMAFRWVTEFCPNAKYVMKTD TDVFIN  
TGNLVKYLLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPFYCSGLGYIMSRD  
LVPRIYEMMGHVKPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHLDVCQLRRVIAAHG  
FSSKEIITFWQVMLRNTTCHY

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**FIGURE 138**

CCTCTGTCCACTGCTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT  
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA  
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA  
ATAACAACGGATGGGACTCCTGGAATTCATCTGGGATTATGGAAATGGCTTGTCTGCAACC  
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT  
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC  
CTCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA  
AAAAACATTGCAAACATGTGTCGTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC  
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTAATGATGAGATTGTGGACATTT  
CCTTCTGTGGAGACACGGTGGAGAACTTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT  
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT  
TTTCTCTACTAGTTATGTTGATTCTTTAAGTTCAATAAAATCATTAGCATTGAAAAAA

**FIGURE 139**

MKFTIIVFAGLLGVFLAPALANYNINVNDDNNNAGSGQGSVSVNNEHNVANVDNNGGWDWSNS  
 IWDYGNNGFAATRFLQKKTICIVHKMNKEVMPSIQSLDALVKEKKLQGGKPGGPPPKGLMYSVN  
 PNKVDLDSKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

**FIGURE 140**

CATTTCTGAAACTAATCGTGTGAGAATTGACTTTGAAAAGCATTGCTTTTTACAGAAGTATA  
 TTAACTTTTTAGGAGTAATTTCTAGTTTGATTGTAATATGAAATAATTTAAAGGGCTTCG  
 CTCATATATAGGAAAATCGCATATGGTCCTAGTATTAAATCTTATTGCTTACTGATTTTTT  
 TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA  
 GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATG  
 CAAGCTTATAGTTGAAATATTTTTCAGGAATTAC**ATGA**ATGACAGTCTTCGAACCAATGTGT  
 TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCACTACCTTGCAAGCTAGAGCACTT  
 CAGATTCGGTTGCCAACTCGTCCCCATTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAAT  
 CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAAACTATGAATTAC  
 TGGAAAAAGAGTAGAAAAAGAAAGTAGCCTTACAAGAAGCCAAATTAAGCAAGGGA  
 TTGAATCCGGATGGAAGTCCAGCCCTTCAACCCTGGGTGGATTTTCTCCAGCCTCCAAGCC  
 ATCATCACCAAGAGAAGTAAAGCTGAAGAGAAATCACCAATCTCCATTAATGTGAAGACAG  
 TCAAAAAGAACCTGAGGATAGACAACAGGCTTCCAAAAGCCCTTACAATGGTGTGAAGAAA  
 GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACG  
 TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA  
 GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTCGAAGACATCATAATCAT  
 GGTTCCTCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAAACAGACATGG  
 TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGATCACTCAGATGCAG  
 CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT  
 GAGAGGTCCATAAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG  
**CTGA**CTTTCTCTTCTTTGAGCCTGCATCAGTTCTTGGTTTGCCTATCTACAGTGTGATGT  
 ATGGACTCAATCAAAAACATTAAACGCAAACTGATTAGGATTTGATTTCTTGAAACCTCTA  
 GGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAAAGAACTATGTTAATTTTTTTGCACATT  
 AAAATGCCCTAGCAGTATCTAATTA AAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT  
 TGTGTATTGTTTATTGCTATAAGAACTGGAGCGTGAATTCGTAAAAATGTATCTTATTTTT  
 ATACAGATAAAATTGCAGACACTGTTCTATTTAAGTGGTTATTTGTTTAAATGATGGTGAAT  
 ACTTTCTTAACACTGGTTTGTCTGCATGTGTAAGATTTTTTACAAGGAAATAAAATACAAAT  
 CTTGTTTTTTCTAAAAAAAAAAAAAAAAAAGT

**FIGURE 141**

MNDSLRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLLFGTTEEEIQEICIETLRLY  
TRKKPNYELLEKEVEKRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK  
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSTRSRSRSHTPRRHYN  
NRRSRSGTYSSRSRSHSESPPRRHHNHGSPHLKAKHTRDDLKSSNRHGHKRRKRSRSQ  
SKSRDHSDAAKKHRHERGHHRDRRERSRSFERSHKSKHHGGSRSRSGHGRHR

**FIGURE 142**

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA  
TTTTTTGAANNATTATCGGGTCANAATTGNCCTTGAAAAGCATTGCTTTTACAGAAATATAT  
TANCTTTTtagagtaatttctagtttgattgtaatatgaaattattttaaagggcttcgct  
CATATATAGGAAAATCGCATATGGTCCTAGTATTAATNTTATTGCTTACTGATTTTTTTG  
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA  
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATGCA  
AGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT  
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA  
GATTCCGTTGCCAACTNGTCCCCATTGGTTTCTTCTTTTGGTACTACAGAAGAGGAAATCC  
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTACTG  
GAAAAAGAAGTAGAAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTTAAAGCAAAGGGATT  
GAATCCGGATGGAACCTCAGCCCTTTCAACCCTGGGTGGATTTTCTCC

**FIGURE 143**

GGCACGAGGCTCGTGCCAAGCTTGGCACGAGGGTGACACGCGTTCTCGCACGCGT**CATGGC**  
GGTCTCGGAGTACAGCTGGTGGTGACCCGTGCTACTGCCACCCTCATGCACAGGCTGGCGC  
CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTTTGTTCGGATACAAGCACCCG  
TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG  
GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCCGAGATGCCCCGTTCCAGCTGG  
AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGCTTCTTCCTGGAGTACCAGTGG  
TTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTTCACAGAGGCCACTACTACAT  
GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCACGGTGACCTTCT  
CCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGGTGAGCGC  
TCTGTCTGCCTCACCTTTGCCTTCTCTTCTGCTGCTGGCCATGTGCGGTGCAAGTGGTGCG  
GGAGGAGACCCTCGAGCTGGGCCTGGAGCCTGGTCTGGCCAGCATGACCCAGAAGTTAGAGC  
CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCTGTGGCCAAGCTGGCTATCCGCGTG  
GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCTCACCTTCCAGGCCTGCGGCTGGC  
CCAGACCCACCGGGACGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCTCCTGTC  
ACACCAGCTTCTGTCTCCCTGTTTCATCCTGTGGCTCTGGACAAAGCCCATTGCACGGGAC  
TTCTGCAACAGCCGCCGTTTGGGGAGACGCGTTTTCTCCCTGCTGTCCGATTCTGCCTTCGA  
CTCTGGGCGCCTCTGGTTGCTGGTGGTGTGTGCCTGCTGCGGCTGGCGGTGACCCGGCCCC  
ACCTGCAGGCCTACCTGTGCCTGGCCAAGGCCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC  
CGCATCGAAGCCCGTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT  
GAGCTTGCAGTACCTGACGCCGCTCATCCTCACCCCTCAACTGCACACTTCTGCTCAAGACGC  
TGGGAGGCTATTCTCGGGCCTGGGCCAGCTCCTCTACTATCCCCGACCCATCCTCAGCC  
AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCGACGCGGATTGCCGG  
GGCCCTGGGTGGCTGCTTACTCCCTCTTCTCCGTGGCGTCTGGCCTACCTCATCTGGT  
GGACGGCTGCCTGCCAGTGCTCGCCAGCCTTTTCGGCCTCTACTTCCACCAGCACTTGGCA  
GGCTCC**TAG**CTGCCTGCAGACCCCTCTGGGGCCCTGAGGTCTGTTCTGGGCAGCGGGACA  
CTAGCCTGCCCCCTCTGTTTGCGCCCCGTGTCCCAGCTGCAAGGTGGGGCCGGAATCCCC  
GGCGTTCCTTTCACACAGTGCTGACCCGCGGCCCCCTTGGACGCCGAGTTTCTGCCTCA  
GAACTGTCTCTCTGGGCCAGCAGCATGAGGGTCCCGAGGCCATTGTCTCCGAAGCGTATG  
TGCCAGGTTTGTAGTGGCGAGGGTGATGCTGGCTGCTCTTCTGAACAAATAAAGGAGCATGCC  
GATTTTTAA





**FIGURE 145**

CGTTNGCACGCGTCAATGGCGGTCCTCGGAGTACAGCTGGTGGTGACCCCTGCTCACTGCCAC  
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTT  
TGTTCCGATACAAGCACCCGTNTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC  
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC  
GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGC  
TTCTTCTGGAGTACCAGTGGTTTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTT  
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT  
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTTGACAGTGACACGGCTGTACTTCAGC  
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTTGCCTTCTCTTCTGCTGCTGGC  
CATGCTGGTGCAAGCG



**FIGURE 147**

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTAT  
APSEPVSAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSEGRSNRTRARPFERSTIRSR  
FKKINRALSVLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITSIKINRVDP  
SESLSIRLVGGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLL  
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVKVDPEGV  
FIFNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQVRS  
PDIFQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHRE  
WDLPIYVISVEPGGVISRDGRIKTGDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEV  
KEYEPQEDCSSPAALDSNHNMAPSDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIV  
GGYEEYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHACLARLLKELKGRI  
TLTIVSWPGTFL

**FIGURE 148**

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT  
GCACAGGGCAGCTTTACTTACTCCAGCACCTTCTCTCCCAGGCAAATGGTGCTGACCATCT  
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC  
AATGTTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC  
AGGATCATGCTCTTCTACCACAATTTTGGACTATAAACATGGCTACATTGCATCCAGGGTGC  
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT  
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG  
GGTCAAGTACAACCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTAC  
CCATTGAGAACTCTGCAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT  
AATGTGCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG  
TGCAGACATTCATGTTTAGGATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCC  
TTGGTTTACTCAAAAGTCAAATTAAATTCCTTCCCAATGCCCCAACTAATTTTGAGATT  
AGTCAGAAAATATAAATGCTGTATTATA

**FIGURE 149**

MKILVAFLVVLTI FGIQSHGYEVFNII SPSPNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT  
IFDYKHGYIASRVLSRRACFILKMDHQNIPLNNLQWYIYEKQALDNMFSNKYTWWKYNP  
LESLIKDVDWFLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

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**FIGURE 150**

GGCACGAGCCAGGAAGTCTAGGAGGTTCTCACTGCCCCGAGCAGAGGCCCTACACCCACCGAGGC  
**ATG**GGGCTCCCTGGGCTGTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG  
GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCCTGGAAGTTTCCCCAAAG  
GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCATCACCTATTCCCTC  
TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCCTCCTT  
CAACCTCAACGTCACACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT  
CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG  
CCAGTGTCTGAGCTGCGGGCCAACCTTCACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGGA  
GATGATCTGCCAGGCGTCCTCGGGCAGCCCCACCTATCACCAACAGCCTGATCGGGAAGGATG  
GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCCTGCCG  
AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAACAACGCCAATGTCCAGCACAGCGC  
CCTCACAGTGGTGCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCCTGGAGA  
GCCCCATCCTTGCCCTTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTGGG  
GGGTTCAGGATAGGAATGGGGAGGTGAGAGGACGCAAAGCAGCAGCCATG**TAGA**AATGAACC  
GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTCGTATTGGGA  
GTTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 151**

MGLPGLFCLAVLAASSEFSKAREEEITPVVSIAYKVLEVPKGRWVLITCCAPQPPPPITYSL  
CGTKNIKVAKKVVKTHEPASFNLNVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK  
PVSELNANFTLQDRGAGPRVEMICQASSGSPFITNSLIGKDGQVHLQQRPCHRPANFSFLP  
SQTSDWFWCQAANNANVQHSALTVVPPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG  
GFRIGNGEVRGRKAAAM

### **Signal Peptide:**

amino acids 1-18

### **N-glycosylation Sites:**

amino acids 86-89, 132-135, 181-184

GGTCTCTTAATGCGCAGCAGCCGCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG  
CTGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCTCACTCTCTTTGCTATGACATCACCGT  
CATCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAA  
CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCAACCTGTCACTCCCTGGGGAAGAAA  
CTAAATGTCAACGGCCTGGAAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACT  
TACAGAGCAACTGCGTGACATTCAGCTGGAGAATTACACACCCAAGGAACCCCTACCCCTGC  
AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT  
TTCGATGGGCAGATCTTCTCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC  
TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCTTCCATT  
ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCAC  
TGGAGCCAAAGTGCAGGAGCACCCTCGCCATGTCTCAGGCACAACCCAACCTCAGGGCCAC  
AGCCACCACCTCATCTTTTGCTGCCTCCTCATCATCTCCCTGCTTATCTTCCCTGGCA  
TCTGAGGAGAGTCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCAG  
GTCTTGATCAAACCTCGCCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGTATGTCCAGT  
GGCCTCCAGCAGATCATGATGACATCATGGACCAATAGCTCATTCACTGCCTTGATTCTCT  
TTGCCAACAAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGTACC  
TGATGGAATTCCTGCACTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTC  
TCTTTTGTTTGAAAATCAAGTACTTCTTTGAATGATGATCTCTTCTTGCAAAATGATATT  
GTCAGTAAAAATAATCACGTTAGACTTCAGACCTCTGGGGATTCTTCCGTGTCTGAAAGAG  
AATTTTAAATATTATTAATAAGAAAAAATTTATATTAATGATTGTTTCTTTAGTAATTTAT  
TGTTCTGTACTGATATTTAAATAAAGAGTCTATTTCCCAAAAAAAAAAAAAAAAAAAAA



**FIGURE 153**

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVI PKFRPGPRWCAVQGQVDEKTF L  
HYDCGNKTVTPVSP LGKKLVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR  
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFS  
MGDCIGWLEDFLMGMDSTLEFSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

**Important features:****Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 224-246

**N-glycosylation site.**

amino acids 68-72, 82-86

**N-myristoylation site.**

amino acids 200-206, 210-216

**Amidation site.**

amino acids 77-81

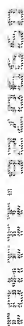
**FIGURE 154**

GGGAAAGCCATTTTCGAAAACCCATCTATACAACTATATATTTTCATTCTGCTGCTAGCTG  
CCTTGGGCCTCACAATTTTCATTCTGTTTTCTGACTTTCAAGTTATATACCGTGGAATGGAG  
TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTTGGTGGTAGCCCTCACCCAATTCTG  
GTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAAATCATGAACTCTGGCTGTTGATCAAAA  
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC  
TCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAAATGGATTCTACAT  
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTTGGGAGGCCAAC  
CCACAGAACAGCATTTCTGGGCCAGGCTGTAATCAGAATTGTCGTCGTACATGCTCAACAGC  
ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCTTACCTTT  
CCTCTCTCCATTCAAGCATTCAAAGTATATTTCAATGAATTAAACCTTGAGCAAGGGACC  
TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATTTCTGTAT  
CATCCTTTTCAATAAACTGTATTCATTTTGAIAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 155**

MELIPTITSWRVLIIVALTQFWCGFLCRGFHLQNHLLIKREFGFYSKSYRTWQKKLA  
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGGOPTQHFWARL



STTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAAATTATGAACGTGCCACACCAATGAAG  
CTCTTTGGGAGGTAACCTGTGCACACCAACCTGGAAATGCCATCTCTCGCTCCCGCTCGCTCA  
CCTCACGGCGCAAGTGTGTGATTCTGTGTGACAGCCATCGCTGCTCGCCCTCAGCGGCGCCC  
AGAACTGCCCTCCGTTTGCTCGTGCAGTAACCACTTCAGCAAGGTGGTGTGCACGCGCCGG  
GGCCTCTCCGAGGTCCCGCAGGGTATTCCTCGAACACCCGGTACCTCAACCTCATGGAGAA  
CAACATCCAGATGATCCAGCGCGACACCTTCGCGACCTCCACCACTCGGAGGTCTCGAGT  
TGGGCAGGAACCTCCATCCGGCAGATTGAGGTGGGGGCCCTTCAACGGCCTGGCCAGCCTCAA  
ACCTTGGAGCTGTTGCAGAACTGGTGACAGTCACTCCCTAGCGGGGCCCTTTGAATACCTGTC  
AAGCTCGGGGAGCTCTGGCTTGTGCAACACCCCATCGAAAGCATCCCTCTTACGCTCTTCA  
ACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT  
GAGGGAGCTTTTGAAGGGCTGTTCAACCTCAAGTATCTGAACCTTGGGCATGTGCAACATATA  
AGACATGCCAACTCTACCCCGCTGTTGGGGCTGGAGGAGCTGAGATGTCAAGGAACCACT  
TCCCTGAGATCAGGCCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTCA  
TGCAACAGCTCAGCTGATTGAGCGGAATGCTTTTGAAGCGGGTGGCTCTCACTGTGGAACT  
CAACTTGGGCCCAATAACCTCTCTTCTTTGGCCCATGACCTCTTACCCCGCTGAGGTACC  
TGGTGGAGTTGCATCTACACCACAACCTTGGAACTGTGATTGTGACATTCTGTGGCTAGCC  
TGATGGCTTCGAGAGTATATACCCACCAATTGCCACTGCTGTGGCCCTGTGATGCTCCCAT  
GCATATCGAGAGCGCGTACTCTGTGGAGTGTGACAGGCTCCTTCCAGTGCTCTGCCCT  
TCATCATGGACGCACCTCGAGACCTCAACATTTCTGAGGGTGGATGGCAGAACTTAAGTGT  
CGGACTCCCCCTATGTCCTCTCGTAAGTGGTGCTGCCCAATGGGACAGTGTCTGACCGCTC  
CTCCGCGCACCAAGGATCTGTGCTTCAACGACAGCAACCTTGAACCTTCCACGTGCTG  
TTTCAGACACTGGGGGTGACACATGCATGGTGACCAATGTTGCAGGCAACTCCAACGCCCTCG  
GCCTACTCTAATGTGAGCAGCGGTGAGCTTAAACACTCAACTACAGCTTCTTCCACCACT  
AACAGTGGAGGACCGAGAGATCTCGCTGAGGACAGCAACGCGAAAGTACAAGGCTGTCTTCA  
CCAGTCCACTGGTTACCAGCGGCATATACCACCTCTACCACGCTGCTATTGAGACTAC  
CGTGTGGCCAGCAGGTGGAGTACCCGCGACAGACCACTGCAAGATGCGAGACAGCT  
GGATGAAGTCAATGAAGACCACAAGATCATCATTTGGCTGCTTTGGCAGTGAATCTGCTAG  
CTGCCGCCATGTTGATTGTCTTCTATAAATCTCGTAAGCGGCACCAGCAGCGGAGTACAGT  
ACAGCGCCCGGAGTGTGGAGATAATCCAGGTGAGCAGAGACATCCGACGAGCAACTCCG  
AGCAGCAACAGCAGCTCCGTCGGTGATACAGTGTGAGGGGCGATAGTGTGCCACAATCT  
ATGACCATAATTAACATAACACCTACAACCAGGCATGTGGGCCCACTGGACAGAAACAGC  
CTGGGAATCTCTGACACCCACAGTCACCACTATCTGAACTTATATAATTCAGACCCA  
TACCAGGACAGAGTGAAGGAACTCAAATATGACTCTCCCTCCCCAAAAAACTATATAAAT  
GCAATAGAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTTCTTGTA  
TATGCTTATATATTAAGTCTATGGCTGTTTAAAAAAACAGATATATATAAATTTAAAGA  
CAAAAAGCTCAAAACA

**FIGURE 157**

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAASAGPQNCPSVCSCSNQFSKVVCT  
RRGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS  
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY  
ISEGAFEGFLFNLKYLNIGMCNIKDMPNLTPLVGLEELEMMSGNHFFEIRPGSFHGLSSLKKLW  
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLPDHLFTPLRYLVELHLHHPWNCDCDILW  
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL  
KCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGVYTCMVTNVAGNSN  
ASAYLVNSTAELNTSNYSFFTFTVTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ  
TTRVPKQVAVPATDTTDKMQTSLDEVMTTKIIIGCFVAVTLLAAAMLIVFYKLKRHQQRS  
TVTAARTVEIIQVDEDI PAATSAAATAAPSGVSGEGAVVLPTIHDHINYNTYKPAHGAHWTE  
NSLGNSLHPTVTITISEPYIIQTHTKDKVQETQI

**FIGURE 158**

CGCTCGGGCACCAGCCGCGGCAAGG**ATG**GAGCTGGGTTGCTGGACGCAGTTGGGGCTCACTTTTCTTCAGCTCC  
 TTCTCATCTCGTCCCTGCCCAAGAGAGTACACAGTCATTAATGAAGCCTGCCCTGGAGCAGAGTGGAAATATCATG  
 TGTCCGGAGTGCTGTGAATATGATCAGATTGAGTGCGTCTGCCCCGGAAAGAGGGAAGTCGTGGGTTATACCAT  
 CCCTTGCTGCAGGAATGAGGAGAATGAGTGTGACTCCTGCCTGATCCACCCAGGTTGTACATCTTTGAAAAC  
 GCAAGAGCTGCCGAATGGCTCATGGGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAG  
 TGCCGAGCAGGCTGGTACGGAGGAGACTGCATGCGATGTGGCCAGGTTCTGCGAGCCCCAAAGGGTCAGATTTT  
 GTTGGAAAGCTATCCCTAAATGCTCACTGTGAATGGACCATTATGCTAAACCTGGGTTTGTATCCAACATAA  
 GATTTGTGATGTTGAGTCTGGAGTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTTCGTGATGGAGACAAC  
 CGCGATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATCCTCACT  
 CCACGTCCTCTTCCACTCCGATGGCTCCAAGAATTTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGCAT  
 GCTCCTCATCCCTTGTTTCCATGACGGCAGCTGCGTCTTTGACAAGGCTGGATCTTACAAGTGTGCTGCTTG  
 GCAGGCTATACTGGGCAGCGCTGTGAAAATCTCCTTGAGAAAGAAACTGCTCAGACCTGGGGGCCAGTCAA  
 TGGGTACCCAGAAAATAACAGGGGGCCCTGGGCTTATCAACGGACGCCATGCTAAAATTGGCACCTGGTGTCTT  
 TCTTTGTAACTCCTATGTTCTTAGTGGCAATGAGAAAGAACTGCCAGCAGAATGGAGAGTGGTCAGGG  
 AAACAGCCCATCTGCATAAAAGCCTGCCAGAACCAAGATTTACAGCTGGTGAGAAGGAGAGTTCTCCGAT  
 GCAGGTTCACTCAAGGGAGACACCATTAACACAGCTATACTCAGCGGCCTTCAGCAAGCAGAACTGCAGAGTG  
 CCCCTACCAAGAAGCCAGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGCTCCAG  
 TATGAGTGCACTCACCTTCTACCGCCGCTGGGCAGCAGCAGGAGGACATGCTGAGGACTGGGAAGTGGAG  
 TGGGCGGGCACCATCCTGCATCCTATCTCGGGGAAAATTGAGAACATCACTGCTCCAAGACCCAAAGGTTGC  
 GCTGGCCGTGGCAGGCAGCCATCTACAGGAGGACCGCGGGTGCATGACGGCAGCTACACAAGGGAGCGTGG  
 TTCTAGTCTGACGCGGTGCCCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCCACTGTGTACTGACCTGGG  
 GAAGGTCACCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAAATTCTACCGGGATGATGACCGGGATG  
 AGAAGACCATCCAGAGCCTACAGATTTCTGCTATCATCTTGCATCCCAACTATGACCCCATCTGCTTGATGCT  
 GACATCGCCATCCTGAAGCTCCTAGACAGGCCCCGTATCAGCACCCGAGTCCAGCCCATCTGCCTCGCTGCCAG  
 TCGGGATCTCAGCACTTCTTCCAGGAGTCCACATCACTGTGGCTGGCTGGAATGTCTGGCAGACGTGAGGA  
 GCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGGTGGTCAGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAG  
 CATGAGGACCATGGCATCCAGTGAGTGTCACTGATAACATGTTCTGTGCCAGCTGGGAACCCACTGCCCTTC  
 TGATATCTGCACTGCAGAGACAGGAGCATCGCGGCTGTCTCTCCCGGACGAGCATCTCCTGAGCCACGCT  
 GGCATCTGATGGGACTGGTCAGCTGGAGCTATGATAAAACATGCAGGCCAGGCTTCCACTGCCTTCAACAG  
 GTGCTGCCTTTAAAGACTGGATTGAAAGAAATATGAAAT**TGA**ACCATGCTATGCACTCCTTGAGAAGTGTTTC  
 TGTATATCCGTCTGTACGTGTGTCATTGCGTGAAGCAGTGTGGGCCGTAAGTGTGATTGGGCTGTGAACCTGG  
 CTGTGCCAGGGCTTCTGACTTCAGGGACAAAACCTCAGTGAAGGCTGAGTAGACCTCCATTGCTGGTAGGCTGAT  
 GCCGCGTCCACTACTAGGACAGCCAATTGGAAGATGCCAGGGCTTGCAAGAAGTAAGTTTCTTCAAAGAAGACC  
 ATATACAAAACCTCTCCACTCCACTGACCTGGTGGTCTTCCCAACTTTTCAGTTATACGAATGCCATCAGCTTG  
 ACCAGGGAAGATCTGGGCTTCATGAGGCCCTTTTGGGCTCTCAAGTTCTAGAGAGCTGCCTGTGGGACAGCC  
 CAGGGCAGCAGAGCTGGGATGTGGTGCATGCCCTTTGTGTACATGGCCACAGTACAGCTCTGGTCTTTTCTTCC  
 CCATCTCTTGTACACATTTTAATAAAATAAGGGTTGGCTTCTGAACACAAAAA  
 AA  
 AA

**FIGURE 159**

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENWIMCRECCEYDQIECVCPGKREVV  
GYTIPCCRNEENECDSCLIHGCTIFENCKSCRNGSWGGLTDDFYVKGFYCAECRAGWYGGD  
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD  
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDG  
TCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV  
VSFFCNSYVLSGNEKRTCQONGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLH  
QLYSAAFSKQKLQSAPTKKPALPFGDLPBGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK  
WSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNE  
RTVVVAHCVTDLGKVTMIKTADLVVLGKFYRDDDRDEKTIQSLQISAILLHPNYDPILLD  
ADIAILKLLDKARISTRVQPICLAASRDLSFSQESHITVAGWNVLADVRSPGFKNDTLRSG  
VVSVDLSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPS DICTAETGGIAAVSFPGRASPEPR  
WHLMGLVSWSYDKTCSHRLSTAFTKVLFPKDWIERNMK

**FIGURE 160**

ACCAGGCATGTATCTTCAGTTGTCTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGA  
 AGCTTTCTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGC  
 TTCAACCTGACTTTCCACCTTTCTACAAATTCCGATTACTGTTGCTGTTGACTTTGTGCCT  
 GACAGTGGTTGGTGGGCCACCAGTAACTACTTCGTGGGTGCCATTCAAGAGATTCCATAAG  
 CAAAGGAGTTCATGGCTAATTTCCATAAGACCCTCATTTTGGGGAAGGGAAAACTCTGACT  
 AATGAAGCATCCACGAAGAAGGTAGAACTTGACAACGTGCTCTTCTGTGCTCCTTACCTCAG  
 AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAAATC  
 CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCGCCATC  
 CTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAACATCTGCATCCCTT  
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTATCCACCAGGCTGAAGGTAAAAAGT  
 TTAATCGAGCCAACTCTTGAATGTGGGTATCTAGAAGCCCTCAAGGAAGAAAATTGGGAC  
 TGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA  
 GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG  
 GATATTTTGGGGGTGTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT  
 AACAACCTACTGGGGATGGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAG  
 AATGAAAATTTCCCGGCCCTGCCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAG  
 ACAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTCAGAGTCTGG  
 AGAACAGATGGGTTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA  
 TATCAACATCACAGTGGAATTTCTGGTTTGGTGCATGACCCTGGATCTTTTGGTGATGTTTGG  
 AAGAACTGATTCTTTGTTTGAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA  
 AGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTTCTTTTGTATTTTCTTAGCAGAGCT  
 CCTGGTGATGTAGGTATAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGATCATG  
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAGGATGACTCAAAGGAT  
 AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATAT  
 TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGCTGAGAGAACCAGAGTTGTTCT  
 CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTTCATTTATCCTGTACAATCATCT  
 GTGAAGTGGTGGTGTCAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCA  
 GGACACAGTGAACCTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGGCTGCAAAGGCAG  
 CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCT  
 TCCAGTGATGCCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAAATGA  
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAATAATAATAATA  
 TGTCTATCAAAACCTCTGTAGTAAAATGTGAAAAGCAAAA



**FIGURE 161**

MGFNLTfHLSYKFRLLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLILGKGKT  
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVAENPKVSRGRYRPQECKALQRV  
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEEN  
WDCFIFHDVDLVPENDFNLYKCEEHPKHLVVGRRNSTGYRLRYSGYFGGVTTALSREQFFKVNG  
FSNNYWGWWGGEDDDLRLRVELQRMKISRPLPEVGKYTEVFTTRDKGNEVNAERMKLLHQVSR  
VVRTDGLSSCSYKLVSVENHPYINITVDFWFGE

**Important features:****Signal peptide:**

amino acids 1-27

**N-glycosylation sites:**

amino acids 4-7, 220-223 and 335-338

**Xylose isomerase proteins:**

amino acids 191-201

**FIGURE 162**

CGTGGGCCGGGGTTCGCGCAGCGGGCTGTGGGCGCGCCCGGAGGAGCGACCGCCGAGTTCTC  
 GAGCTCCAGCTGCATTCCCTCCGCGTCCGCCCCAGCCTTCTCCGCTCCGGGCCCCGCA**AATG**  
 GCCCAGGCAGTGTGGTTCGCGCTCGGCCGCATCCTCTGGCTTGCTGCTCCTGCCCTGGGC  
 CCGGCAGGGGTGGCCGAGGCTGTATGAACCTCAATCTCACCACCGATAGCCCTGCCACCA  
 CGGGAGCGGTGGTGACCATCTCGGCCAGCCTGGTGGCCAAGGACAACGGCAGCCTGGCCCTG  
 CCCGCTGACGCCCACCTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGCTTACTGGCAA  
 GATGGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTCCGGCCACGTGCCCGGGGAATTCCCGG  
 TCTCTGTCTGGGTCACTGCCGTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTG  
 GTCTCCCCATCACAGAGTTCCTCGTGGGGACCTTGTGTCACCCAAGACACTTCCCTACC  
 CTGGCCAGCTCCTATCTCATAAGACCGTCTGAAAGTCTCCTTCCCTCCACGACCCGA  
 GCAACTTCCTCAAGACCGCCTTGTTTTCTCTACAGCTGGGACTTCGGGGACGGGACCCAGATG  
 GTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGACCTTCACCGTGAAGCT  
 CAAAGTGGTGGCGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGA  
 CCGGGGACTTCTCCGCTCGTGAAGCTGCAGGAACCCCTTCGAGGCATCCAAGTGTGGGG  
 CCCACCTTAATTCAGACCTTCCAAAAGATGACCGTGACCTTGAACTTCTGGGGAGCCCTCC  
 TCTGACTGTGTCTGGCGTCTCAAGCCTGAGTGCTCCCGCTGGAGGAAGGGGAGTGCCACC  
 CTGTGTCGTGGCCAGCACAGCGTACAACCTGACCCACACCTTCAGGGACCTTGGGGACTAC  
 TGCTTCAGCATCCGGGCCGAGAATATCATCAGCAAGACACATCAGTACCACAAGATCCAGGT  
 GTGGCCCTCCAGAATCCAGCCGGCTGTCTTTGCTTTCCCATGTGCTACACTTATCACTGTGA  
 TGTTGGCCTTCATCATGTACATGACCTGCGGAATGCCACTCAGCAAAAGGACATGGTGGAG  
 AACC CGGAGCCACCTCTGGGGTCAAGTGCTGCTGCCAGATGTGCTGTGGGCCTTTCTGTCT  
 GGAGACTCCATCTGAGTACCTGGAATTTGTTCTGTGAGAACCACGGGCTGCTCCCGCCCTCT  
 ATAAGTCTGTCAAACTTACACCGTG**TGA**GCACCTCCCCCTCCCCACCCCATCTCAGTGTAA  
 CTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAGGAGGGGTTTATT  
 TGCGTGGGGCTGTTGGCCTGGATCATCCATCCATCTGTACAGTTTCAGCCACTGCCACAAGCC  
 CCTCCTCTCTGTACCCCTGACCCAGCCATTCACCCATCTGTACAGTCCAGCCACTGACA  
 TAAGCCCCACTCGGTTACCACCCCTTGACCCCTACCTTTGAAGAGGCTTCGTGCAGGACT  
 TTGATGCTTGGGGTGTCCGTGTTGACTCCTAGGTGGGCTGGCTGCCACTGCCCATTCCT  
 CTCATATTGGCACATCTGCTGTCCATTTGGGGGTTCTCAGTTTCTCCCCAGACAGCCCTAC  
 CTGTGCCAGAGAGCTAGAAAGAAGGTATAAAGGGTTAAAAATCCATAACTAAAGGTTGTAC  
 ACATAGATGGGCACACTCACAGAGAGAAGTGTGCATGTACACACACCACACACACACACA  
 CACACACACACAGAAATATAAACACATGCGTCACATGGGCATTTAGATGATCAGCTCTGTA  
 TCTGGTTAAGTCGGTTGCTGGGATGCACCTGCACATAGAGCTGAAAGGAAATTTGACCTCCA  
 AGCAGCCTGACAGGTTCTGGGCCCGGGCCCTCCCTTTGTGCTTTGTCTCTGAGTTCTTGC  
 GCCCTTTATAAGGCCATCCTAGTCCCTGCTGGCTGGCAGGGGCTGGATGGGGGGCAGGACT  
 AATACTGAGTGATTGCAGAGTGCTTTATAAATATACCTTATTTTATCGAAACCCATCTGTG  
 AAATTTTCACTGAGGAAAAGGCTTGACGCGGTAGAAGAGGTTGAGTCAAGGCCGGCGCGG  
 TGGCTCAGCCTGTAATCCCAGACTTTGGGAGGCCGAGCGGGTGGATCACGAGATCAGGA  
 GATCGAGACCACCTGGCTAACACGCTGAAACCCGCTCTCTACTAAAAAATACAAAAAGTT  
 AGCCGGGCTGGTGGTGGGTGCCTGTAGTCCAGCTACTCGGGAGGCTGAGGCAGGAGAATG  
 GTGCGAACCCGGGAGCGGAGCTTGACGTAGCCAGATGGCGCCACTGCACCTCCAGCCTGA  
 GTGACAGAGCGAGACTCTGTCTCCA

**FIGURE 163**

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA  
LPADAHLYRFHWIHTPLVLTKMEKGLSSTIRVVGHVPGFEPPSVVWVTAADCWMCQPVARGE  
VVLPITEFLVGDVLVVTQNTSLPWPSYLTKTVLKVSFLLHDPSNFLKTALFLYSWDFGDGTQ  
MVTEDSVVYYNYSIIIGTFTVKLVVAEWEEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL  
GPTLIQTFQKMTVTNLNFGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDPGD  
YCFSIRAENIISKTHQYHKIQVWPSRIQPAVFAPFCATLITVMLAFIMYMTLRNATQQKDMV  
ENPEPPSGVRCCCMCCGPFLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

**Important features of the protein:****Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 339-362

**N-glycosylation sites.**

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

**FIGURE 164**

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACG**ATG**GCACTGAGCTCCAGATCT  
GGGCCGCTTGCCTCCTGCTCCTCCTCCTCCTCGCCAGCCTGACCACTGGCTCTGTTTTCCCA  
CAACAGACGGGACAACCTTGCAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTG  
GATGCCCATGTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCCATCTGCATTTTCTGCT  
GCGGCTGCTGTCATCGATCAAAGTGTGGGATGTGCTGCAAGACG**TAGA**ACCTACCTGCCCTG  
CCCCGTCCCCTCCCTTCCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGAATAAAA  
TGGCTGGTTCTTTTGTTCCTCAA  
AAA



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## **FIGURE 165**

MALSSQIWAACLLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH  
FPICIFCCGCCHRSKCGMCCCKT

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MALSSQIWAACLLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH  
FPICIFCCGCCHRSKCGMCCCKT

**FIGURE 166**

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGC  
 CTGGATCTTCCACC**ATG**TTCCCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC  
 ATCTCCCTGACTGTCTCTTACCCCTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTTGG  
 AGTCTCCTTTGGTATCCGCAAACTCTACATGAAAAGTCTGTTAAAAATCTTTGCGTGGGCTA  
 CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCACCAGCTTTACAAAGCCCTACACCAAC  
 GGAATCATTGCAAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTCTGTCGAAGTGG  
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCC  
 GAAAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTG  
 GAGTCTTGAACTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC  
 GGTCTGTGGGGTTAGGAGTGCTGATTTCGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC  
 TGGCTTTCACAGGGATTAGCCTTCTGGTGGTGGGCACAACGTGGTGGGATACTTGCCAAAT  
 GGGAGGTTTAAAGAAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGGC  
 AGCGCTGACAGCCATCATCACTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCT  
 GTGTGGCCAATCATACCTCACCGATCGATGTGATCATCTTGCCAGCGATGGCTATTATGCC  
 ATGTTGGGTCAAGTGGCACGGGGGACTCATGGGTGTGATTTCAGAGAGCCATGGTGAAGGCCCTG  
 CCCACACGTCTGGTTTTGAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA  
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCATCTCATCTTCCCAGAAGGAACCTGCATC  
 AATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTGAATTTGGAGCCACAGTTTACCC  
 TGTGCTATCAAGTATGACCCTCAATTTGGCGATGCCCTTCTGGAACAGCAGCAAAATACGGGA  
 TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTG  
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAATCTGC  
 CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCCCTGAAGAGGGAGAAGG  
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAAACCAC  
 AAGGACAGGAGCCGCTCT**TGA**GCCTGCCTCCAGCTGGCTGGGGCCACCGTGGGGGTGCCAA  
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCACTGCTGTGCTTCCAGACTCCAGGG  
 CTCCCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTCCGCCGAGCCGAGCGGGATCCCTGT  
 GCACCCGGCGCAGCCTACCCTTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGA  
 CGAGATGCCCTGTTTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAAGTGAACCTCCCCA  
 CCTTTGCACGCTGTGGGGCTGAGTGGTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGAT  
 GGCGGTACAAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGGGCGGCCACCCG  
 CTCCTCCAGGAAAGGCACAGCTGAGGCCACTGTGGCTGGCTTCGGCCTCAACATCGCCCCAGC  
 CTTGGAGCTCTGCAGACATGATAGGAAGGAACTGTCACTCTGCAGGGGCTTTTCAGCAAAATG  
 AAGGGTTAGATTTTTATGCTGCTGCTGATGGGGTTACTAAAGGGAGGGGAAGAGGCCAGGTG  
 GGCGCTGACTGGGCCACTGGGGAGAACGTGTGTTCTGTACTCCAGGCTAACCTGAACTCCCC  
 ATGTGATGCGCGCTTTGTTGAATGTGTGCTCGGTTTCCCCATCTGTAATATGAGTCGGGGG  
 GAATGGTGGTGATTCTACCTCACAGGGCTGTTGTGGGGATTAAAGTGCTGCGGGTGAGTGA  
 AGGACACATCAGTTCAGTGTTTTCAAGTACAGGCCCAAAAACGGGCACGGCAGGCCCTGAG  
 CTCAGAGCTGCTGCATGGGCTTTGGATTTGTCTTGTGAGTAAATAAACTGGCTGGTGAA  
 TGA

660736  
 123456789  
 101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIVPAIFGVSVFGIRKLYMKSLLKIFAWATLRME  
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRS GSSKALDNTPEFELSDIFYFCRK GME  
TIMDDEVTKRFSAEELSWNLLSRTNYNFQYISLRLTVLWGLGV LIRYCFLPLRIALFTG  
ISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRALTAIITYHDRENRPNGGICVANH  
TSPIDV IILASDGYAMVGQVHGGMLMGV IQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ  
DKSKLPILIFPEGTCINNTSVMMPFKKGSFEIGATVYPVAIKYDQFGDAFWNSSKYGMV TYL  
LRMMTSWAIVCSVWYLP PMTTREADEAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTF  
KEEQQKLYSKMIVGNHKDRSR

**FIGURE 168**

GCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGGACCCCTGGCCCTCA  
CGTCTCCTCCAGGGATGGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCCTCCAC  
ACCTGGCAGGCCCAGGCTGTTCCCAACCATCCTGCCCCTGGGCCTGGCTCCAGACACCTTTGA  
CGATACCTATGTGGGTGTGTCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG  
AAATGGCCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCAGGAGACCTGGGAGGAC  
AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGT  
CTACACCAACTCATCGAACACCTTGTA TGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG  
GCTCCCGGGAGCTCTACATGAGGCACTTTCCCTTCAAAGGCCCTGCATTTCTACCTGATCCGG  
GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTTCG  
AGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT  
TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTTGGGGAGAAGAGCGGGGCTGT  
GTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCTCCTCTCTGCCCCCTG  
GAAGACTCTGCTCTTGGCCCCCTGGAGAGTTCCAGCTCTCAGGGGTGGGCCCTGAAGTCCA  
ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG  
CAGCCTTGAGAAGCAAGAACATGGTTCGGACCCAGCCCTAGCAGCCTTCTCCCCAACCAGG  
ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACCTCTGCTATGTGATGGGGACTTCCT  
GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA  
TGGAGTTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA



MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGC AEEMEEKAAPLLKEEMAHH  
ALLRESWEAAQETWEDKRRGLTLPFGFKAQNGIAIMVYTNSSNTLYWELNQAVRTGGGSREL  
YMRHFFPKALHFYLIRALQLLRSGGCSRGPGEVVFVRGVSLRFEPKRLGDSVRLGQFASSS  
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPWKTL LLLAPGEFQLSGVGP

**FIGURE 170**

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCA  
CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG  
GTCGGTTCGGTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC  
TATTGTCTGGACCTTCAACACAACCCTCTTGTACCATACAGCCAGAAGGGGGCACTATCA  
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAG  
CTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT  
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG  
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG  
GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC  
CCATAATGGGTCCATCCTCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT  
GCGTTGCCAGGAACCTGTGAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT  
GAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCTCCTGTGTCTCCTGTTGGTGCCCT  
CCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG  
AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGCGGAAACTCCTAACATATGCCCCAT  
TCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAATCCTAAAGGAAGA  
TCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAAAGATGGAAAATCCCCACTCAC  
TGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGCAGTG  
CACTCCCCTAAGTCTCTGCTCA

**FIGURE 171**

MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT  
IQPEGGTIIIVTQNRNRERVDFFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV  
YEHLSPKPKVTMGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW  
GESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLW  
FLKRERQEEYIEKKRVDICRETPNICPHSGENTHEYDTIPHTNRTILKEDPANTVYSTVEIP  
KKMENPHSLLTMPDTPRLFAYENVI

**FIGURE 172**

CTGGTTCCCCAACATGCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC  
TCTGGACCCGTGAAAGAGCTGGTCGGTTCGGTTGGTGGGGCCGTGACTTTCCCCTGAAGTC  
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAC  
AGCCAGAAGGGGGC~~ACT~~ATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA  
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT  
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG  
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG  
ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT  
GGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAG  
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCTGTGCAGCAGAACTTCTCAAGCCCC  
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCTCCT  
GTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTC  
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGGAA  
ACTCCTAACATATGCCCCCATCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA  
TAGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAA  
AGATGGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAG  
AATGTTATCTAGACAGCAGTGCACCTCCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAA

**FIGURE 173**

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAAGATGCTGCTGCT  
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGAAGGA  
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA  
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCTTGAGAA  
TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG  
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT  
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAAACGAAAAGGATGGGA  
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA  
GGTTTGCACAACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT  
GCCAATCGCTGCCTCCAGGCCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTTGAGTGGAC  
ACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCCAGTATAAATTC  
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCCAGTCTATCAACATGTTACC  
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCCTTGACAAT  
TTTTCATGAAATTATTCCTCTTCCTGTTCAATAAATGATTACCCTTGCACTTAA

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**FIGURE 174**

MKMLLLLCGLTLVCVHAAEEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ  
IHVLENSLVLVKVTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI  
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

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MKMLLLLCGLTLVCVHAAEEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ  
IHVLENSLVLVKVTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI  
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA  
TGGATTACGCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG  
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTC  
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG  
AAAAAGAGCGTGCTGCAACAACAGAAGTGAATGTTTCTTTCATCATTTTTTCAGTGTGATCA  
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAGGTCCTCTC  
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA  
CATTTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTCGACCTCCTACTG  
GTTTTCAATAAAACCCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC  
TTCGATTCTGAAGAAAAACAACATAGGCTTATCCACTTCTCAGTATTTTTAGGTCTATTGCT  
TGTTGGAATTCTGGAGGTCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTC  
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTA  
TCAGTAGTTTGAAAAA

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**FIGURE 176**

MTCCEGWTS CNGFSLLV LLLLGVVLNAIPLIVSLVEEDQFSQNPISC FEWWFPGIIGAGLMA  
IPATMSLTARKRACCNRTGMFLSSFFSVITVIGALYCLISIQALLKGPLMCN SPSNSNA  
NCEFS LKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRL  
IHFSVFLG LLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

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**FIGURE 178**

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEV  
KHCTDQISFKRRLSLKKSWWK

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**FIGURE 179**

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG  
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG  
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTC  
GAACTGTGACATGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG  
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG  
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG  
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC  
TCATCACTCCAGGCTCTGCCACTACTTGCTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA  
AGCCTAACACTGGCCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC  
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAACTCG  
CCCCACCACCCCTCA

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**FIGURE 180**

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAAGIAAVLSGKCK  
YKSSQKQHSPVPEKAIPLITPGSATTC

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGG**ATG**TCGCTGCTGAGCCTGCC  
TGGCTGGGCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC  
CTGGCTACTCGCCCGCATCTGTGGCTTGGACCTATGCCTTCTATAACAACCTGCCGCCGGCTCC  
AGTGTTCCTCCACAGCCCCCAAAACGGAAGCTGGTTTTGGGGTCACTGGGCCTGATCACTCCT  
ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTGCGCCACCTATTCCAGGGCTTTACGGT  
ATGGCTGGGTCCCATCATCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCA  
CCAATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAAGCCCTGG  
CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCGCCACCGTCGGATGCTGAC  
GCCCGCCTTCCATTTCAACATCTGAAGTCCTATATAACGATCTTCAACAAGAGTGCAAAACA  
TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAG  
CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG  
TCAGGAGAGGGCCAGTGAATATATTGCCACCATCTTGGAGCTCAGTGCCCTTGTAGAGAAAA  
GAAGCCAGCATATCTCCAGCACATGGACTTTCTGTATTACCTCTCCCATGACGGGCGGCGC  
TTCCACAGGGCCTGCCGCCTGGTGCATGACTTCACAGACGCTGTCATCCGGGAGCGGCGCTCG  
CACCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG  
ATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTGATGAGGAT  
ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC  
CTGGTCTGTACAACCTTTCGAGGCCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC  
AAGAGCTTCTGAAGGACCGCATCTAAAGAGATTGAATGGGACGACCTGGCCAGCTGCC  
TTCCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCG  
ATGCTGACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAGGCATTACCTGCC  
TCATCGATATTATAGGGGTCCATCACAACCCAACCTGTGTGGCCGATCTGAGGTCTACGAC  
CCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCCTTTCTC  
CGCAGGGCCAGGAAGTGCATCGGGCAGCGCTTCGCCATGGCGGAGATGAAAGTGGTCTGG  
CGTTGATGCTGCTGCACTTCCGTTTCTGCCAGACCACACTGAGCCCGCAGGAAGCTGGAA  
TTGATCATGCGCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCTGAATGTAGGCTTGCA  
GTGACTTTCTGACCCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGGTGTGTCAA

**FIGURE 182**

MSLLSLPWLGLRPVAMSPWLLLLLVGSWLLARILAWTYAFYNNCRRLQCFPQPPKRNWFWG  
HLGLITPTEEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLF  
IRFLKPWLGEKILLSGGDKWSRHRMLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGS  
SRLDMEHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY  
LSHDGRRFHRACRLVHDFTDVIRERRRTLPTQGIDDFKDKAKSKTLDFIDVLLLSKDEDG  
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCQEVEQLLKDRDPKEIEW  
DDLAQLPFLTMCVKESSLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW  
PDPEVYDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT  
EPRRKLELIMRAEGGLWLRVEPLNVGLQ



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**FIGURE 184**

MYKLASCCLLFTGFLNPLL~~SL~~PLLD~~S~~REISFQLSAPHEDARLTPEELERASLLQILPEMLGA  
ERGDILRKADSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

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MYKLASCCLLFTGFLNPLL~~SL~~PLLD~~S~~REISFQLSAPHEDARLTPEELERASLLQILPEMLGA  
ERGDILRKADSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV



**FIGURE 185**

GAACATTTTTAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT  
GGGGTTGCTGGTTTAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA  
CCACCTCCGCCAGGAAGTGCAGGCCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCC  
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT  
CCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGAGTCGAAGAAGCCACCA  
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCCGAAGATGGAGGTCAAGCAGA  
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT  
CAGGGGTTCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG  
GAAGAGGCCAAAGAGGCCCCAGCCGACAAGTGATCGCCACAAGCCTTACTCACCTCTCTCT  
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTGTGA  
CAAGCTCAGGAGGCGAATAAATGTTCAAACGTGA

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**FIGURE 186**

MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG  
GQAEGAEDLEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

**FIGURE 187**

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCTCGTCCAGTACCTC  
 GTGAACCCCGGGTCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGCTGCTGT  
 TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCTGATAGTCGTGATCATCGGGATGCTCGTG  
 CTCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT  
 GAGTATGTCCCCACCCCTAAGCCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATC  
 TTACACCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCACGCCTGGGGCCAGAGCTTTT  
 GTCCCCGTGTGCGCATGTGTTTACGGGTGAGCCTCTCCAGAAGTGAGATCATGGACAAAAA  
 GGGCAAATCACAGGAAGAAATTAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC  
 TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAATGTTTCAGA  
 GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT  
 CAAAAACACAAGTAGAAATTCTAACAAATGAAATATATTACAGGCAGGTCAACCCTAACA  
 AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTC  
 AGTCATGTTGCTGAACGACGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT  
 AACAAACACCTCCCTGCTCCTGGCACCAGCCGTTTTGGTCATGGTGGGCCAGCTGCAAAGCG  
 TCTTCCATTCTCTGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGAC  
 ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA  
 ACCCTTGGTCAGGGCAGAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGA  
 GCATCCCCCTGCCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCACCAAGA  
 GCCTCCTTGTTTCATAACCACAGGTTACCCTACAAACCACTGTCCCCACACAACCTTGGGGAT  
 GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCTGAGGGTTGA  
 ATTTTAAAAACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCTGAGGGTTGA  
 ATTTTAAAAACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCTGAGGGTTGA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

MNTWLLFLPLFPVQVQLTIIVIIIGMLVLLLDLFLGLVHLGQLLIIFIHYLSMSPTLSPRSPQGW  
VVRAAHLTPLLEYVNPNEPPTPGARVFPVRVRCSGSASPRSEIMDKKGKSQEEIKSMRTQQ  
AQQEAEELTPRPAGVVPGA

**FIGURE 189**

GAGTGCAGATGGCATCCTTCGGTTCCTCCAGACAAGCTGCAAGACGCTGACCATGGCCCAAG  
 ATGGAGCTCTCGAAGGCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT  
 ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG  
 TGCCCAAGCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTG  
 GATGGAGATACCAACACATCCACCAGGAGGTGGTACAATACAACTGGGAGACTGGGGATG  
 CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAG  
 AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACCTTACACCACCAGCCAAGAGAGGTGAGAAA  
 GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTACCCCCACTCTCCGATTTGGAGGGAA  
 GCGGTTGATGGAGAAGGCTTCCCTCCCCTCCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTA  
 TGGTTATCCTCGGGAACGCGATCACCTACATCGGACTTCAATTATCAGCTTCTCTCTGCT  
 ACTAACAGACTTGCTACTCACTGGGAACCTGCTGTGGGCTCAAACCTGAGCGCCTTTGCTG  
 CTGTTTCTCTGTCTGTCTGTCAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAAGTC  
 TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGAATTATGGCTG  
 GGCCTTCTACATGGCCTGGCTCTCCTTCACCTGCTGCATGGCGTCGGCTGTACCACCTTCA  
 ACACGTACACCAGGATGGTGCTGGAGTTCAAGTGCAAGCATAGTAAAGAGCTTCAAGGAAAAAC  
 CCGAACTGCCTACCACATCACCATCAGTGTTTCCCTCGCGGGCTGTCAAGTGCAGCCCCCAC  
 CGTGGGTCTTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG  
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGATTTCAAAGAGGGGCCAGCCAGGAGCTG  
 AAAGAAGCAGTTAGGTCACTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGGA  
 GTAGGCTTGAGCCCTACCTTACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG  
 TCTCTTGAGCATGGTTTTTATAGAGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC  
 CTAAGGGATTCTGGGTGCCACTGCTCTCTTTTCCCTCTACAGCTCCATCTTGTTTCACCCAC  
 CCCACATCTCACACATCCAGAATTCCTTCTTTACTGATAGTTTCTGTGCCAGGTTCTGGGC  
 TAAACCATGGAGATAAAAAGAAGAGTAAATAACACTTCCCGACCTTAAGGATCTGAA

**FIGURE 190**

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP  
VSLDGDNTNSTQEYVQYNWETGDDRFSSFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR  
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQL  
PPATNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSDCQLGSRRLTTCLE  
LWLGLLHGLALLHLLHGVGCHHLQHVVHQDGAGVQVQA

**FIGURE 191**

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCAGATGTGGTTACCCCTTGGTCTCCTG  
 TCTTTATGTCTTTCTCCTCTTCTATTCTGTTCATCTCCCTCACTTAAGTCTCAGGCCTGTCA  
 GCAGCTCCTGTGGACATTGCCATCCCCTCTGGTAGCCTTCAGAGCAACAGGACAACCTATG  
 TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT  
 GATCTCTATGACAGAGCCACTTCTCCACCCTGAAATGTTCCCTGCTCTGAAATCTGGCATG  
 AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCTGCCCTATTCTCCTCCCAA  
 GTCTGTTCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAG  
 CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT  
 AGCCACCTCCTGTGTCAGCCAGTATTAACATGTCCCCTTCCCCCTGCCCCGCCGTAGATTCA  
 GACATTCGCCCCTGTGTGCCACCAAAACCAGGACTTCCCCCTGGCTTGGCATCCCTGGCTCT  
 CTCCTGGTACCCAGCAAGACGTCTGTTCAGGGCAGTGTAGCATCTTCAAGCTCCGTTACT  
 ATGGCGATGGCCATGATGTTACAATCCCCTGCTGAATAATCAAGTGGGAAGGGAAGCA  
 GAGGGAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCCTGAGGAAAAACAAA  
 GGGGAAGCAACAGGAACCTTCTGCAACTGGTTTTTATCGGAAGATCATCCTGCCTGCAGATGC  
 TGTGTAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAA  
 ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTCTGATTCCAAACCTTTTATTACTTTGGG  
 AAGTCACTCAGCCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGG  
 AACCAAGGAAACTAACAATGTAGTTACTAGTGAATACCCAATGGTTTCTCCAATTATGCC  
 CATGCCACCAAAACAATAAAACAAAATTCTCTAACACTGAAA

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## **FIGURE 192**

MWLPLGLLSLCLSPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGME  
HRNHLCFCDLYDRATSPPLKCSLL

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MWLPLGLLSLCLSPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGME  
HRNHLCFCDLYDRATSPPLKCSLL



**FIGURE 193**

GTAGCGCGTCTTGGGTCTCCCGGCTGCCGCTGCTGCCGCCGCCGCTCGGGTCTGGAGCCAGGAGCGACGTCA  
 CCGCC**ATG**CGCAGGCATCAAAGCTTTGATTAGTTTGTCTTTGGAGGAGCAATCGGACTGATTTTTTGTATGCTT  
 GGATGGCCCTTCCAATATAGACAATACTGGCCCTCTTTGTTCTATTTTTTACATCCCTTTACCATTTTCC  
 ATACTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAAGCTTGTGAAGAACTTGCCTCTTTT  
 TTACAAACGGGCATTGTCGTGTACGCTTTTGGACTCCCTATTGTATTTGCCAGAGCACATCTGATTGAGTGGGGA  
 GCTTGTGCACCTGTTCTCACAGGAAACACAGTCATCTTTGCAACTATACAGGCTTTTCTTGGTCTTTGGAAG  
 CAATGACGACTTCAGCTGGCAGCAGTGG**TGA**AAAGAAATTAAGTGAACCTATTGTCAAAATGGACTTCCTGTCA  
 GTTGGCCATTACGCACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCCTTTGGGGGTATTTTA  
 GGTGCTCCCTCTCACCTTTTATTGTAAGCATACTATTTTACAGAGACTTGTGTAAGGATTAAGGATTTTCT  
 CTTTTGAAAAGCTTGACTGATTTTACACCTTATCTATAGTATGCTTTTGTGGTGCTTCTGCTGAATTTAAATAT  
 TTATGTGTTTTTCTGTAGGTTGATTTTTTTTGGAAATCAATATGCAATGTTAAACACTTTTTTAAATGTAATCA  
 TTTGCATTGGTTAGGAATTCAGAAATTCGCCCGGCTCTATTACTGGTCAAGTACATCTTTTCTCTTAAAAATTTAT  
 TAGCCTCCATTATTACAAAAAATTATAAAAAAAGTTTTCAGTCAGTCAGGATGACATCACTCCCAATGTTATG  
 CAGACATACAGACGGTTGGCATACGTTATAGACTGTATACCTCAGTCGAAATATAGCTGCATTATACCTCAGAG  
 GGGCCAAAGTGTAAATGCCCATGCCCTCCGTTAAGGGTTGTTGGTTTTACTGGTAGACAGATGTTTTGTGGATTG  
 AAAATTATTTTTATGGAATTGCTACAGAGGAGTGCTTTTCTCAATTGTTAGAAGAATTTATGTTAAACTTTA  
 AGGTAAGGGTGAAAAACATTTTTGAGATAAGGTTTTTATTTATGTTTATTATGTTAGAGTGAGTTGCAATGT  
 GGGGAAGAAATGACATTGAAATTCAGTTTTTGAATCCTGTTTCTATTATAAGTGAAATTTGTGATCTCCCTATC  
 AACCTTTCATGTTTACCTGTTAAAAATGGACATACATGGAACCACTACTGATGAGGGACAGTTGTATGTTTGC  
 ATCATATATGCCAGAAAACTTCTCTGCTTCTCCTTTTGACTTATTTGGTATGTTGTATATATTACATAAAA  
 TAACTTTTCAAAATATAGTTTAAATACACTTAGAAGTGTTTACTTACCTGGAATAATGCTATGCCGTACATT  
 CAGAGTGCCCCCTCCCCTGCAAGGCCTTGCCATGATTAACAAGTAACTTGTTAGTCTTACAGATAATTTCATGCA  
 TTAACAGTTTAAGATTTAGACCATGGTAATAGTAGTTCATTCTCTAAGGTTATATCATATGTAATTTAAAG  
 TATTTTTAAGACAAGTTTCCTGTATACCTCTGAACTGTTTGTATTTGAGTTTATCATGATAGATCTGCTGTTT  
 CCTTATAAAGGCATTTTGTGTGAGTTAATGCAAGTAGCCAAAGTCCAGCTATATAGCAGCTTCAGAAACAT  
 ACCTGACCAAAAAATTCACAGTAACAGGCATGATCAATTTATAGTGGTCTGTTTACATCTAATAATTTATCAGGA  
 CTTTTTTCAGGATGGGTTATAAAAAACATTCAAGTTGGTCTGACAGTATTTTGTAAAGGATATTTGTTTGTATG  
 TTTATTCAGTATACTTACATAAAAAATTATTTGCCATCAGCCAAAACCTCAGTAATCATGACAGCTGTCTGTGT  
 TTTATGAAGTTTATTTCTCAGAAAAATGGGAATAAAATTTGGGATTTGTTGAGCTTTTTTACTAAAGATGCTTAA  
 AGCCACAGGTTTTATTTGCTTAAGCCATGACTTTAGATATGAGATGACGGGAACAGGACGAATATCG  
 GCGTGTGGCTGGAGCCTCCCACTGGAGGCTGAAGTGGCTTGTGATTTATAATGTTTCAAGAGGAA  
 GGTGCAAGGTACACATGAGTTAGAGAGCTGGTGAGACAGTTGGGAACCTTTTGTGCTTGTGATCTACTGGACTTT  
 TTTTTGCAAGAGTGCAATCTCTGGTCTTCCCTATTTTCTGTTCTGGATGTCAGTGCAAGTGCAGTCTGACTG  
 TTTTATCCACTTGGCCACAGACTTTTCTAACAGCTGCGTATTATTTCTATATACTAAATGCATTGGCAGCATT  
 GTGTCTTTGACCTTGATACTAGCTTGACATAGTGTCTGCTCTGATTTCTAGGCTAGTTACTTGAGATATGAAT  
 TTTCCATAGAATATGACCTGATACAACTATACCATTCTCTATGGAAGAAAACTTTTGTATGATGAACAATAA  
 AGATTTTAAATATCTATTTTAAAAA



[illegible]

**FIGURE 196**

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH  
NLSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNNHICSVQGDADFQKLRRVKELTLSSNQ  
ITQLPNTTFRMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRI FQDCRS  
LKFLDIGYNQLKSLARNSFAGLFKLTTELHLEHNDLVKVNFAHFPRILSLHSLCLRRNKVAIV  
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRIILNSWKSLSIT  
LAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVYAFHLCEDGA EPTSG  
HLLSAVTNRSDLGPPASSATTLADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVGTMA  
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNH  
IEGALVIINEYGSCTCHQQPARECEV

**FIGURE 197**

GTGCAAGGAGCCGAGGCGAGATGGGCGTCCTGGGCCGGGTCTGCTGTGGCTGCAGCTCTGC  
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAA  
CTGGAGCCAGAACCGGACCCCGTGCGCCGGCGCGCCGTTGAGTTCCCGCGGACAAGATGG  
TGTCAGTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA  
CTCGTCCTGGCTTCAGGAGCCGGATTTCGGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG  
CGCGGGCGAACCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT  
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGGCCTGCCGC  
CACGACGACGTCTTCTTTCCGCCTAGTGCCTCCTTCCGCGTGGGGCTCGGCCCTGGCGCTAG  
CCCCGTGCGTGTCCGAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG  
CTGTTTTCTGGCGTCCCGCGGGGCCGCTACGCTTCACGGGCCGGGCGCGTTGAGCGTG  
GGCCCCGAGGACTGCGCGGACCCGTGGGCTGCGTCTGCGGCAACGCGGAGGCGCAGCCGTG  
GATCTGCGCGGCCCTGCTCCAGCCCCT



**FIGURE 199**

[illegible]

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**FIGURE 200**

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYLSFIP  
FARDAVKKCFVCLA

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**FIGURE 202**

MTSKFILVSFILAALSLSLSTTFSLQLDQQKVLVLSFDGFRWDYLYKVPTPHFHYIMKYGVHVK  
QVTNVFITKTPYNHYTLVTLGLFAENHGIVANDMFDPIRNXSFSLDHMNIYDSKFWEETPIW  
ITNQRAHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY  
WEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITS DHGMTQCSEER  
LIELDQYLDKDHYTELIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN  
SRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD  
LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYF  
IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLQA

**Signal Peptide:**

amino acids 1-22

**Transmembrane Domain:**

amino acids 429-452

**N-glycosylation sites:**

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-  
372, 382-385, 389-392

**Somatomedin B Domain:**

amino acids 69-85

**Sulfatase protein Region:**

amino acids 212-241

**FIGURE 203**

GGATTTTTGTGATCCGCGATTTCGCTCCACGGGCGGGACCTTTGTAAGTGCAGGAGGCCAG  
 GACAGGCCACCCCTGCGGGCGGGAGGCAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGC  
 AGAGAGGCCAAGCCCTTGCTTGGGTACACAGCCAAAGGAGGCAGAGCCAGAACTCACA  
 CCAGATCCAGAGGCAACAGGGAC**ATG**CCACCTGGGACGAAAAGGCAGTCACCCGCAGGGCC  
 AAGGTGGCTCCCGTGAGAGGATGAGCAAGTTCTTAAGGCACTTCACGGTCGTGGGAGACGA  
 CTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGG  
 AGCAGCCACCACCACACCACTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCTGACGTTGCC  
 CCTGCCCCCTGGCCCCGCACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAAACTGTT  
 CAGCTCCACAGGTTTCAGGTCATCATCTGCTTGGTGGTCTGGATGCCCTCCTGGTG  
 TTGCTGAGCTCATCTGGACCTGAAGATCATCCAGCCCGACAAGAATAACTATGCTGCCATG  
 GTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCTTTAAATT  
 ATTTGTCTTCCGCTGAGTTCTTTCACCACAAGTTTGAGATCCTGGATGCCGTCGTGGTGG  
 TGGTCTCATTCATCTGGACATTGTCTCCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGC  
 CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCGGATCATCAATGGGATTATCATCTCAGT  
 TAAGACACGTTCAGAACGGCAACTCTTAAGGTTAAACAGATGAATGTACAATTGGCCGCCA  
 AGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCCTGGAC**TGA**TGAGTTTGCTGTATC  
 AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT  
 CACACAGCCACCGTGAAAGTCCTGGAGTAAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG  
 CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTA  
 TCACTTCAGATTACAAATCACACAGAGCATCTGCCTGTTTTCAATCACAAGAGAACAAAACC  
 AAAATCTATAAAGATATTCTGAAAAATATGACAGAATTTGACAAATAAAAGCATAAACGTGTA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 204**

MATWDEKAVTRRAKVAPAERM SKFLRHFTVVGDDYHAWNINYKKWENEEEEEEEEQPPPTPV  
SGEEGRAAAPDVAPAGPAPRAPLDFRGMLRKLFSSHRFQVIIICLVVLDALLVLAELIDL  
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLSSTSLRSWMPVVVVVSFILDI  
VLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLLRKQMNVLAAKIQHLEFS  
CSEKPLD



**FIGURE 206**

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD  
LDGQLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEI MQSLRDLGVKISEQQAEKILK  
SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW  
WRHLVAGGGAGAVSRTCTAPLDRLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGI  
NVLKIAPESAIKFMAEQIKRLVGSDQETLRIHERLVAGSLAGAIQSSIYPMEVLKTRMAL  
RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNS  
ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG  
LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

**Important features:****Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 284-304, 339-360, 376-394

**Mitochondrial energy transfer proteins signature.**

amino acids 206-215, 300-309

**N-glycosylation site.**

amino acids 129-133, 169-173

**Elongation Factor-hand calcium-binding protein.**

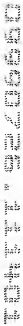
amino acids 54-73, 85-104, 121-140

**FIGURE 207**

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCC**AT**  
**GC**CTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTTCTGGCTGGAG  
 CAATTGCACTCATCATTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTC  
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAA  
 ACTTCTGTATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA  
 AAGAAGGCCAAAGATGAGCTGTCGGAGCAGGATGAAATGTTTCAGAGGCCGGACAGCAGTGTTT  
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGC  
 TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA  
 AAATGAGGCTTTCAGCATGCCGGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG  
 CGGTGTGAGGCTCCCCGATGGTTCCCCCAGCCACAGTGGTCTGGGCATCCCAAGTTGACCA  
 GGGAGCCAACCTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACCTTGAGAATGTGACCA  
 TGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAA  
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAGGCGGAG  
 TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGTCTCTTCTTTCTTTGCCATCAGCT  
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAA**TAA**TGTGCCTTGGCCACAAAAAAG  
 CATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTACCACCAGATATGACCTAG  
 TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAGAGCA  
 AGAAACAAAAAGAAGCCAAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAA  
 GACATATTAGAAGTTGGGAAAATAATTCATGTGAAGTAGACAAGTGTGTTAAGAGTGATAAG  
 TAAATGCACGTGGAGACAAGTGCATCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCT  
 GGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTATGTTATATGTGCTG  
 TAATGTTGCTCTGAGGAAGCCCTTGAAAGTCTATCCCAACATATCCACATCTTATATTCCA  
 CAAATTAAGCTGTAGTATGTACCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG  
 GCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCT  
 TGGCTTCTCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA  
 ACAGAGCAGTCGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTTAAACAAAAAA  
 AA

**FIGURE 208**

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI  
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRKKNVQLTD  
AGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVD  
QGANFSEVSNTSFELNSENVTMKVSVLYNVTINNTYSCMIENDIAKATGDIKVTETSEIKRR  
SHLQLLNSKASLCVSSFFAISWALLPLSPYMLK





**FIGURE 209**

[illegible]

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**FIGURE 210**

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPFLL  
LNQCGSLLYLTLASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGS  
RHTCVSSFPEFISPEWVRTRPFPILPFPLQLFCFLVAIRVPFPWTVVRKTEAGVWD

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MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPFLL  
LNQCGSLLYLTLASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGS  
RHTCVSSFPEFISPEWVRTRPFPILPFPLQLFCFLVAIRVPFPWTVVRKTEAGVWD

**FIGURE 211**

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG  
 GAAGATGACAGCAATTATAGCAGGACCCCTGCCAGGCTGTGCGAAAAGATTCCGCAATAAAACT  
 TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT  
 TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCATGAAGGGCATCCTCG  
 TTGCTGGTATCACTGCAGTGCTTGTGTCAGCTGTAGAATCTCTGAGCTGCGTGCAAGTGAAT  
 TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG  
 CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT  
 TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCT  
 GCTGAAGAACTTTTCAATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG  
 CGATGCCCTGGACCCCTCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTATG  
 AATCTAATGGAATTCCTGTCTGGGAAGCCCTGGAAATGCTATGAAGAAGAACAGTGTGTC  
 TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTT  
 CAACGTCAGTAACGCCACCTGTCAGTTCTGTCTGGTGAAAAACAAGACTCTTGAGGAGTCA  
 TCTTTCGAAAGTTTGAGTGTGCAAATGTAAACAGCTTAACCCCCACGTCTGCACCAACCACT  
 TCCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGCCCTTGCCAGCCTCCTTCTTCG  
 GGGACTGCTGCCCAGGCTGCTGGGCTGCACTTTGCCAGCACCCCATTTCTGCTTCTCTG  
 AGGTCCAGAGCACCCCTGCGGTGCTGACACCCTCTTCCCTGCTGCCCCGTTTAACTGC  
 CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTCTTCATTATTA  
 AAGCACTGGTTCATTCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAA



**FIGURE 213**

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCA  
 GGGCTTGCTCTACTGGCCACCCTCCCAACCCCAAGAGCCCAGCCCCATGTCCCCGCCGCCG  
 GCGCGCTGCTGTGGGTCTGCTGCTGAATCTGGGTCCCCGGGCGGCGGGGCCCAAGGCCTG  
 ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCATGACCCGCAG  
 CTACCGGAGCACCGCCCGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA  
 ATGATGCCATGGCCGACGCCGACCGCCTGGCTGGACCAGCGGCTGCCGAGCTCTTGCCCGCC  
 ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGA  
 GGGGGTTGTGATTAATGCCGGAAAGGATAGCACCAGCAGAGAGCTTCCCAGTGCGACTCCCA  
 ATACAGCGGGGAGTTCCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG  
 ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC  
 CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTCACCCTCACCCACAG  
 CCATGCCATCTCCTGAGGATCTGCGGCTGGTGCTGATGCCCTGGGGCCCGTGGCACTGCCAC  
 TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTTCCGGGCGCCT  
 TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAAGCCTTGACCTATCAACAATGTC  
 CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT  
 GCCTCTCAGAGCACCACCAGTACCAGGACCACCACTACCCCTTCCCCACCATCCACCTCAG  
 AAGCAGTCCCAGCCTGCCACCCGCCAGCCCCTGCCAGCCCTGGCTTTTTGGAAACGGGTCA  
 GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA  
 GACAGAAACCAGAGGTAATGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT  
 CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTGTAGTACAGAAAAACAAAACCTGGAAAA  
 CACAA



**FIGURE 215**

CCGGGTCGACCCACGCGTCCGGGGAGAAAGCATGGCCGCGCCTGGCGGCGCGGTTGGTCTCTGCTAGCTGGGGCA  
 GCGGCGCTGGCGAGGGGTCCACAGGGGACCGGTGAGCCGGTGTACCGGCACTGCGTACTGCAAGTGGCAAGAGCA  
 GAACTGCTCTGGGGCGCTCTGAATCACTTCCGCTCCCGCCAGCCAACTACATGAGTCTAGCAGGCTGGACCT  
 GTCGGGACGACTGTAAGTATGAGTGATGTGGGTCACCGTTGGGCTTACCTCCAGGAAGGTCACAAAGTGCCT  
 CAGTTCCATGGCAAGTGGCCCTTCTCCCGTTCTGTTCTTTCAAGAGCCGGCATCGGCCGTGGCCCTCGTTTCT  
 CAATGGCCTGGCCAGCCTGGTGATGCTCTGCCGCTACCGCACCTTCGTGCCAGCCTCCTCCCCATGTACCACA  
 CCTGTGTGGCCTTCGCTGGGTGTCCCTCAATGCATGGTTCGTGTCCACAGTCTTCCACACCAGGGACACTGAC  
 CTCACAGAGAAAATGGACTACTTCTGTGCCCTCCACTGTCATCCTACACTCAATCTACCTGTGCTGCGTCAGGAC  
 CGTGGGGTCTGACGACCCAGCTGTGGTCAGTGCCCTCCGGGCTCTCCTGCTGCTCATGCTGACCGTGACGCTCT  
 CCTACCTGAGCCTCATCCGCTTCGACTATGGCTACAACTGGTGGCCAAAGTGGCTATTGGCCCTGGTCAACGTG  
 GTGTGGTGGCTGGCCTGGTGCTGTGGAAACAGCGGCGGCTGCCTCAGGTGCGCAAGTGCGGTGGTGGTGGTCTT  
 GCTGCTGACAGGGGCTGTCCCTGCTCGAGCTGCTGACTTCCCACCGCTCTTCTGGGTCTGGATGCCATGCCA  
 TCTGGCAGATCAGCACCATCCCTGTCCACGTCCTCTTTTTCAGCTTTCTGGAAGATGACAGCCTGTACCTGCTG  
 AAGGAATCAGAGGACAAGTTCAGCTGGACTGAAGACCTTGGAGCGAGTCTGCCCCAGTGGGGATCCTGCCCCC  
 GCCCTGCTGGCCCTCCCTTCTCCCTCAACCTTGAGATGATTTTCTCTTTTCAACTTCTTGAACCTTGGACATGA  
 AGGATGTGGGGCCAGAATCATGTGGCCAGCCCAACCCCTGTTGGCCCTCACCAGCCTTGGAGTCTGTTCTAGGG  
 AAGGCCTCCAGCATCTGGGACTCGAGAGTGGGCGAGCCCTCTACCTCCTGGAGCTGAAGTGGGGTGGAACTGA  
 GTGTGTTCTTAGCTCTACCGGGAGGACAGCTGGCTGTTTCTCCCAACAGCCTCCTCCCCATCCCCAGCTG  
 CCTGGCTGGGTCTGAAGCCCTCTGTCTACCTGGGAGACCAGGGACACAGGCCTTAGGGATACAGGGGGTCCC  
 CTCTCTGTTACCAACCCCAACCTCCTCCAGGACACCACTAGGTGGTGCTGGATGCTTCTTTGGCCAGCCAA  
 GGTTCACGGCGATTCTCCCATGGGATCTTGAGGACCAAGCTGCTGGGATTGGGAAGGAGTTTCAACCTGACC  
 GTTGCCCTAGCCAGGTTCCAGGAGGGCTCACCATACCTCCCTTTCAGGGCCAGGGCTCCAGCAAGCCAGGGCA  
 AGGATCCTGTGCTGCTGTGTTGAGAGCCTGCCACCGTGTGTCGGGAGTGTGGGCCAGGCTGAGTGCATAGG  
 TGACAGGGCCGTGAGCATGGCCCTGGGTGTGTGTGAGCTCAGGCCATAGTGCAGTGTGGAGACGGGTGTTGT  
 CGGGGAAGAGGTGTGGCTTCAAAGTGTGTGTGTGTCAGGGGGTGGGTGTGTAGCGTGGGTAGGGGAACGTGTG  
 TGCCGCTGCTGTGGGCATGTGAGATGAGTGACTGCCGGTGAATGTGTCCACAGTTGAGAGGTTGGAGCAGAT  
 GAGGGAATCCTGTCAACCATCAATAACTTGTGGAGCGCCAGCTCTGCCCAAGACGCCAAGTGGGCGGACAGC  
 CAGGAGCTCTCCATGGCCAGGCTGCCTGTGTGCATGTTCCCTGTCTGGTGCCCTTTGCCGCCCTCCTGCAAC  
 CTCACAGGGTCCCCACACAACAGTGCCTCCAGAAGCAGCCCTCGGAGGCAGAGGAAGGAAAAATGGGGATGGC  
 TGGGGCTCTCTCCATCCTCCTTTCTCCTTGCCTTCGCATGGCTGGCCTTCCCCTCAAAACCTCCATTCCCCT  
 GCTGCCAGCCCTTTGCCATAGCCTGATTTTGGGAGGAGGAAGGGCGATTGAGGGAGAAGGGGAGAAAGCT  
 TATGGCTGGGTCTGGTTTCTTCCCTTCCAGAGGGTCTTACTGTTCCAGGTTGGCCCAAGGGCAGGCGAGGGGCC  
 ACACATATGCTGTGCCCTGGTAAAGGTGACCCCTGCCATTACACAGCAGCCTGGCATGTTCTGCCCAACAGG  
 AATAGAATGGAGGAGCTCCAGAACTTTCCATCCCAAGGCAGTCTCCGTGGTTGAAGCAGACTGGATTTTG  
 CTCTGCCCTGACCCCTTGTCCCTTTTGGGGAGGGGAGCTATGCTAGGACTCCAACCTCAGGGACTCGGGTG  
 GCCTGCGCTAGCTCTTTTGATACTGAAAACCTTTAAGGTGGGAGGGTGGCAAGGGATGTGCTTAATAAATCAA  
 TTCCAAGCCTCAAAAAAAAAAAAAAAAAA

**FIGURE 216**

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW  
 TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPF SRFLFFQE PASAVASFLNGLASLVMLCR  
 YRTFVPASSPMYHTCVAFAWVSLNAWFWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR  
 TVGLQHPAVVSAFRALLLMLTVHVSYSLSLIRFDYGYNLVANVAIGLVNVVWVWLAWCLWNQR  
 RLPHVVRKCVVVLLQLGLSLELLLDFPPLFWVLDAAHAIWHISTIPVHVLFFSFLEDDSLYLL  
 KESEDKFKLD

**Important features:****Signal peptide:**

amino acids 1-20

**Transmembrane domains:**

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

**N-glycosylation site.**

amino acids 40-44

**N-myristoylation site.**

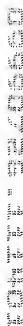
amino acids 43-49

**CUB domain proteins profile.**

amino acids 285-302

**Amiloride-sensitive sodium channels proteins.**

amino acids 162-186





**FIGURE 217**

[illegible]

**FIGURE 218**

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPESSTKETERKETKAEEEL  
DAEVLEVHFPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLK GKRLDINTN  
TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV  
RLINKFNSSSSSLEEKIAALFDLEYVYVHQMDNAQDLLSFGGLQVVINGLNSTEPLVKEYAAF  
VLGAAFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL  
GGLQVLRTLVQEKGTEVLAVRVVTLTYDLVTEKMFEEEEAELTQEMSPEKLQQYRQVHLLPG  
LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCDRYRQDPQLGRTLASLQA EYQVLAS  
LELQDGEDEGYFQELLGSVNSLLKELR

**Important features:****Signal peptide:**

amino acids 1-29

**Hypothetical YJL126w/YLR351c/yhcX family protein.**

amino acids 364-373

**N-glycosylation site.**

amino acids 193-197, 236-240

**N-myristoylation site.**

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

**Homologous region SLS1 protein.**

amino acids 68-340

TTCCGCTTCCGTAGAGGAAGTGGCGCGGACCTTCATTTGGGGTTTCGGTTTCCCCCCCCCTCC  
CTTCCCGGGGTCTGGGGTGACATTGCAACCGGCCCTCTGTTGGGTGCGCTTGCCACCCCCA  
CGCGACATCCCAGCTGGCGCGCCCTCCCAATTTGCGCTGCTCTGGTGCAGGCCCCACCCCC  
TTCCACCTGACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACCTTCGTCGCGTTTCGGC  
CGCGGCTTCCGCTGTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCTCGGT  
CGCAGGGGACATTTTCTGCTGGTCTCCTGCTCTGCCCTCTGTGGTCTGGTGTATCTTTGG  
TCCATGTGACCGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGTCTG  
GTCTCTGTCTCTTACAGGAGGTGTTCGCTTTGCTCATACAAGTGCCTTAAGAAGGCAGA  
TGAAGGTTAGCATCCTGTAGTGAGGACGGAAGATCACCTCATCCCGCAGATGGCTCT  
ATGTTTCTGGTCTCTCTCGGTATCATCAGTGGTGTCTCTCTGTTATCAATATTTGGCT  
GATGCACTTTGGGCAAGGTGTGGTTGGGATCCATGGAGACTCACCTATTACTTCTTGACTTC  
AGCCTTTCTGACAGCAGCCATTATCTGCTCCATACCTTTTGGGAGTGTGTTCTTTGATG  
CCTGTGAGAGGAGACGGTACTGGGCTTTGGGCTGGTGGTGGGAGTCACTACTGACATCG  
GGACTGACATTTCTGAACCCCTGGTATGAGGCGAGCCTGCTGCCACTATGCACTGCTGT  
TTCCATGGGGCTCTGGGCTTTCATCAGACGTGGAGGTCCTCCGAAGTATTCAGCGCAGCC  
TCTTGTGTAAGGATGCACTACCTGGACTGATCGCTGACAGATCCCACCTGCTGTCACTG  
CCCATGACTGAGCCAGCCCGACGCCGGGTCCATTGCCACATTTCTGTCTCCTTCTCGTG  
GGTCTACCCCACTACTCCAGGGTTTGTGTTTGTCTTGTGACCCCTGAGTCTCAAGCTT  
TACGAGGAGCAGCTCGGTTTGACGCAGTCACTGAGTGGTGGGTTGAATCTGCACTTATCCC  
CACCACCTGGGGACCCCCTTGTTGTGTCCAGGACTCCCCCTGTGTCACTGCTCTGCTCTCAC  
CGTGCCCAAGACTCACTCCCTCCCCCTCTCGAGGCCAGCGGACGAGGACAGTCCGGGTGAT  
GGTGATTTCTGCCCTGCGCATCCCAACCCAGGACTGAGGAACTTGGGGGACCCCTGGGC  
CTGGGGTGCCCCCTGATGTCTCTGCCCCGTATTTCTCCATCTCCAGTTCTGGACAGTGCAG  
GGTGCCAAGAAAGGGACCTAGTTTAGCCATTGCCCTGGAGATGAAATTAATGGAGGCTCAA  
GGATAGATGAGGCTGAGTTTCTAGTACTCCCTCAAGACTGGACATCTGGTCTTTTCTCT  
AGGCTGAGGGGGAACCATTTTGGTGTGATAAATACCCATAAAGCTGCTTTTTTCTTTTTT  
GAGTGGGGGGAGGAGGAGGTATATTGAACCTCTTCAACCTCTTGGGCTATATTTTCTCT  
TCTCGAGTTGCTCCTCATGGCTGGGCTCACTTCGTTCCCTTCTCTTGGTCCCAGACCTT  
GGGGGAAGGAAGCAAGTGCATGTTGGGAACGTGGCATTACTGGAACATAATGTTTTAACTT  
CCTTAACCCAGCAGACTGCTCCTCTCCCCAAGGTGAAGTGGAGGGTCTGTGTGTGAGTGGC  
CACTCCAGACGTGCAGTCCCATGGAGGAGTCACTACCATGACATCGTAGGGAAGGAGG  
GAGATTTTTTGTAGTTTTAATTTGGGTTGGGAGGGGCGGGAGGTTTTCTATAAATGT  
ATCATTTTCTGCTGAGGTTGAGTGTCCATCCTTTAATCAAGGTGATTGTGATTTTGACT  
AATAAAAAAGAAATTTGTAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA  
AAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA



AAGCTGGTTTAAAGGAAGCAGAGGAGGGTTAGATTCTGTTGAGTGAGGACGGAAGATCAACCCA  
 TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT  
 TNTCTGTTATCAATATTTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC  
 TCACCCTATTANTTCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

GACCGACCGTTTCAGATGCCCGGTTCCAGTACGGCTTCCTGATTTTGGTGCTGCTGNTCTG  
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG  
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCCATCCGCCAGATGGCCTATGTTTN  
TGGTNTTTCCTTCGGTATCATCAGTGGTGTTTTNTCTGTTATCAATATTTGGNTGATGCAN  
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCCATTATAATTCCTGAATTCAGCCTTT  
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTTGATGCCTGTGA  
GAGGAG

**FIGURE 223**

NGTTGGAGAAGTGGCGCGGACNTTCATTTGGGGTTTCGGTTTCCCCCTTTCCCTTTCCCG  
GGGTCTGGGGTGACATTGCACGGGCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC  
CCAGNTGGNGCGCCCTTCCCATTTCCTGTCTGGTCAGGCCCCACCCCTTCCCACNTG  
ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTGCGGTTGCGCCCGGCCTTCG  
CGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCCTTATCATCCTGGTCGCAGGGGCA  
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGAC  
CGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGTGCTGTCTGTCTGTC  
TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA  
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG  
TCTCTCCTTCGGTATCATAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTTG  
GGCCAGGTGTGGTTGGGATCCATGGAGACTACCC

**FIGURE 224**

GTAAAAGAAAGTGCCGACCTTCATTGGGGTTTCGGTTCCCCCTTTCCCNNTTCCCCGGGG  
TCTGGGGGTGACATTGCACCGCGCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC  
CAGNTGGCGCGCCCTCCCATTTGCCTGTCTGGTCAGGCCCCACCCCCCTCCACCTGA  
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACTTTCGTGCGGTTGCGGCCCGGCCTTC  
GCGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGGC  
ATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTGGTCCATGTGA  
CCGACCGGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTGGTGCTGCTGTCTCTGTC  
CTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTT  
AGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTG  
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTT  
GGGCCAGGTGTGGTTGGGATCCATGGAGAC











**FIGURE 229**

GCAGTCAGAGACTTCCCTGCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCT  
 TGCTTCCTGAAGTACGTACAGTAGCCCGCGGCCAGGGCAATCCGACCACATTTCACTCT  
 CACCGCTGTAGGAATCCAG**ATG**CAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG  
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC  
 CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCCTGCTGAC  
 TTTGTGCTTGGTGTCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACC  
 AGCTCTCCAATACTGGTCAAGACACCATTCTCAAAATGGAAGAAAGATTAGGAAATACGTCC  
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAAGAGTCTGCAGCATGTGGC  
 TGAAAACTCTGTCTGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG  
 AACAATGGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAG  
 GACTGTAAATATTTCTGCCTTAGTGAAAACCTCTACCATGCTGAAGATAAACAACAAGAAGA  
 CCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTT  
 TGCGCCCTGACAGTGGCAAGGCCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAAGT  
 TTCCATATTATAATAGATGTCACCAGCCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGG  
 GATGATCTTCTCAAAGGACTGCAAGAATGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA  
 TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACT**TGA**TTCCGC  
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT  
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTG  
 TTTCTGTTCAGGATCACCAGCATTCTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACA  
 AGAAGTCTTATTTACATGCCACCAACCAACCTCAGAAACCATAATGTATCTGCCTTCTTG  
 GCTTAGAGATAACTTTTAGCTCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTCAT  
 GTCTTCCTTACACTTGGTGAATAAGAACTTTTGAAGTAGAGGAAATACATTGAGGTAAC  
 ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCAGATTGTACC  
 AGCAATACACAAGGAATCTTTTTGTTGTTTCAGTTCATACTAGTCCCTTCCCAATCCAT  
 CAGTAAAGACCCCATCTGCCTTGTCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG  
 AATCTCAAATCTCAATGCCTTATAAGCATTCCCTCCTGTGTCCATTAAGACTCTGATAATTG  
 TCTCCCCCTCATAGGAATTTCTCCAGGAAAGAAATATATCCCATCTCCGTTTTCATATCAG  
 AACTACCGTCCCCGATATTCCTTCAGAGAGATTAAAGACCAGAAAAAGTGAGCCTCTTCA  
 TCTGCACCTGTAATAGTTTCAGTTCTATTTTCTTCCATTGACCCATATTTATACCTTTTACG  
 GTACTGAAGATTTAATAATAATAAATGTAAATACTGTGAAAA

MQAKYSSTRDMLDDGDTTMSLHQSASATTRHPEPRRTEHRAPSSWTWRPVALTLLTLCLVLL  
IGLAALGLLFFQYYQLSNTGQDITISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE  
LYNKAGAHRCSPCTEQWKWHDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS  
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSRPSRDCVAIILNGMIFSKD  
CKELKRCVCERRAGMVKPESLHVPPETLGECD







**FIGURE 233**

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPPRGNTNAARRP  
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAAKAVRTRYISTELGIRQRLLVAVL  
TSQTTLPTLGAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLE  
QHGDDEFDFFLVPDTTYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG  
VLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCILDATGVGCTGDHEGVHYSHLELSPGEP  
VQEGDPHFRSALTAPVRDPVHMYQLHKAFARAELETTYQEIQELQWEIQNTSHLAVDGDRA  
AAWPVGIPAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLGTALEELN  
RRYHPALRLKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGGRRPLTRRVQLLRPLSRVEI  
LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAATLLLLYEPRQAQ RVA  
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTLFLLAGPDTV L  
TPDFLNRCRMHAISGWQAF FPMHFQAFHPGVAPPQGGPPELGRDTGRFDRQAASEACFYNS  
DYVAARGRLAAASEQEEELLES LDVYELFLHFSSLHVLR AVEPALLQRYRAQTCSARLSEDL  
YHRCLQSVLEGLGSRTQLAMLLFEQE QGNST

**FIGURE 234**

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT  
 TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCTAGTGGAGAAAAGGAGT  
 AGCTATTAGCCAATTCGGCAGGGCCCCGCTTTTAGAAGCTTGATTTCTTTGAAGATGAAAG  
 ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAACTCGGGGCGATTGGCTGGGAA  
 CTGTATCCACCCAAATGTCACCGATTTCTTCCTATGCAGGAAATGAGCAGACCCATCAATAA  
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACCTGGAGGCAAAG  
 AGGGTTGCTCAACGCCCCGCTCATTTGGAACCAATCAGATCTGGGACCTATATAGCGTG  
 GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT  
 TTCCCCGCCCTTGAGACCTGCAGCACCATCTGT**CATG**GGCGGCTGGGCTGTTTGGTTTGAGC  
 GCTCGCCGTCTTTTGGCGGCAGCGCGACGCGAGGGCTCCCGGCCGCCCGCTCCGCTGGGA  
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGGAAGCGGCCCCCAGAAC  
 CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTTGATGAGAAGAACCA  
 GACTCCCATGGTTATGACAAGGACCCCGTTTGGACGTCTGGAACATGCGACTTGTCTCTT  
 CTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA  
 GGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGGC  
 CTTCCCATCATGGAATCCAACCTGCTTCGACCCCAGCAAGATCCAGCTGCCAGAGGATGAG**TG**  
**A**CCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC  
 CTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA



**FIGURE 236**

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCCTTTGGCGGCAGCGGCGACGCGAGGGC  
TCCCGGCCGCCCGCGTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT  
GTGGCGGGAAGCGGCCCCCAGAACCGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGA  
CGAAAAC TTGTATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCCGTTTTGGACG  
TCTGGAACATGCGACTTGTCTTCTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC  
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT  
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAGTCTTCGACCCAGCA  
AGATCCAG

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GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCCTTTGGCGGCAGCGGCGACGCGAGGGC  
TCCCGGCCGCCCGCGTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT  
GTGGCGGGAAGCGGCCCCCAGAACCGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGA  
CGAAAAC TTGTATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCCGTTTTGGACG  
TCTGGAACATGCGACTTGTCTTCTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC  
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT  
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAGTCTTCGACCCAGCA  
AGATCCAG

CGCGGCGGCTATGCGCGCTTGCTCTGTCTCGTCTGTGGCTCTTGGGGCCCGCGCGGTGGTGCCCTGCGAAGCAACCCCAAGCGCAGCGCTGCGGGAGGAACTGTGCATCACCCCGCTGCCCTCGGGGACGTAGCCGCCCACTGATTCAGTTTCGCGACGCGTGGGATTCGGAGCTTACGCGGAAGGAGTGTCCCATTTACAGGCTCTTTTCCCAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGAGCTGTCGACCTGTTCATTCACCAAGGCTTTTGGAGAGCAACGATACGTGGGGCGGACCCCTCTCGAGGGCCCATCAGGTGACAGCTGTGGGTCTGGTTTCCAAGACAGTGTCTACTGATGTGGATTAATCTTTGGAAGGAGCTCAGTAATGTCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGACTCCACCAACACAGTCACTCCCACCTGCCTCTTCAAAACCGCTGGGTCTGGCCAAATGACACTGACCACTGTTCTGCGCTATGTCTGTGCTGCCGCGGAGGTGGTGTGCACGAAACCTCACCCTTGGAAGAGAGCTTGTGCCCTGTAGTTTCCAAGCGAGGCTCTCTGTGCTGTGAAGGCAGATCGTCTGTTTCCACACAGGACTACCACTACCAAGGCAGTGCATATCGCCCTGTGTTTCAGAAATGACAGCTGTAGCTATCTCTGGGAGCTGAGGCAGACCTGTGAGTTGATTTGATGTCCTTATCAGTGGGACGGGAAGAAAGACTGTGCTCTTCGGATGTCTCCGACACCTTACCGGAGCCCTGCGCTTCCAGAGAGCCGAGTCTATFTGGACATCACCACTTACAACGAGACACAGACAGCTTAGAGGTGCACCCACCCCGACCCTACATATCAGGACGTCATCTAGGCCTCGGAAGACCTATGCATCTATGACTGTCTGACACCGGCATGATCAACAACCTCTGAAACCTCAACATCCAGCTCAAGTGAAGAGACCCCAAGAGAATGAGGCCCCCCAGTGGCCTTCTGTGATGCCACGGCTGCTGAGTGGCTATGTGGCTGCAGAAGGGGAGCTGAGCAGCATGCTGTGTACAACCCACCCATACCGGGCTTCCCGGTGCTGCTGCTGAGCAGCGTACCTGTGATCTGCGCTGTATGTGCACACCCCTCACCATCACCTCCAAGGGCAAGGAGAACAACCAAGTTACATCCACTACAGGCTGCCACGAGGACGGCTGCAACCCACCTCTCTGGAGATGCTGATTACGTCGCGGCTTACCTAGTCCCAAGGTTTCCATCTCAAGTTTGAAGCGGGCGCTGCTGAAGTGAGCCAGTACACGCCAGATCCTAACCATGGCTTCTATGTGACGCCATCTGTCTCTACGCGCCCTTGTGCCCCAGTGGTATAGCAGCCAAAGCAAGTGGACTGGAAGAGAGTCCCTCTTCAACAGGCTGTTCCCACTGTCTGTAGTGGCTTACTACTTTTGTGGCGCTTACACGGAGCGCTGCTGGTGAACCTGTCCGACACCGGACTTACAGTGCCTTACAACGTGATCTGCCTACAGCTGCATGTGGTGGCCGCTGTGCTACGGCTCTCTTCTACAATCTCTCACCCGAACTTCCATCAGAGGAGCCCGCAGAGGTGGCCTGGCCAAAGCGGCTGGCCAACTTATCCGGCGCGCCGAGGTGTCCCCCACTCTGATTCTTGCCCTTCCAGCAGCTGACAGTGGCTGCGTTTCTCTCTGGGAGGGGAGCCCAAGGCTGTTCTGCGACTGTGCTCTCTCAGAGTGGCTTTTGAACCAAAGTGGCCTGACACAGGTGAGGGCTACAGCTGTGTTGTCCAGTACAGGAGCCACGACCAATGTGGCATTGTAATTGAAATTAACCTTAGAAATTCATTCTCTCACCTGTAGTGGCCAGCTCTATATTGAGGTGCTCAATAAGCAAAAGTGTCGTGTGGCTGCTGTATTGACAGCAGCAAGAAAGATTTCCATCACCAAGAAAGGTCGGCTGGCAGCACTGGCCAGGAGGTGTGGGTGTGCTACACAGTGTGCTAGTGTGAGTTTACTGTTTGTGGAATAAAACCGCTGTTTCCGTGGAAAAA

**FIGURE 238**

MPLALLVLLLLGPGGWCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY  
RLFPKALGQLISKYSLRELHLSFTQGFWRTYWGPPFLQAPSGAELWVWFQDTVTDVDSWK  
ELSNVLSGIFCASLNFIDSTNTVTPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK  
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCNRNACTSISWELRQTL SVVFD AFITG  
QGKKDWLSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT  
YAIYDLLDTAMINNSRNLNIQLKWKRPPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH  
PYRAFPVLLLDTPWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS  
VTKVSIQFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD  
GSNYFVRLYTEPLLVNLPTPDFSMPYNVICLTCTVVAVCYGSFYNNLTRTFHIEEPRTGGGLA  
KRLANLIRRARGVPPL

**FIGURE 239**

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCCTGGTGG  
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCAGCTGACAACGTACGC  
TGCTTCAAGTCCGATCCTCCCCAGTGTACACAGACCAGGACTGTCTGGGGGAAAGGAAGTG  
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCCCTGTGAAGGAAGTGAAGAAGGAGGAA  
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC  
TCCTCCTCTACCAGGTGTCTCAGAAATGATGCTGGGTCCTTTCTACCTCTGGGGGTCACCTC  
TCACCTTGGCACCTGCCCCCTGAGGGTCCTGAGACTTGGAATATGGAAGAAGCAATACCCAACC  
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAAGAGGAAGAGTCACAAAAAG  
TCCAGACCCAGGGACGGTACTTTCCCTCTCTACCTGGTGTCTCTCCCTAATGCTCATGAAT  
GGACCCCTCATGAATGAAACCAAGTGCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC  
TGCAATGTGTGATCACAGCTAGAAGGCACTGTGAGAGAAGAGAACTGGTCCTCACCAGATG  
CTGAATCTGCTGGTGCCTTGATCTTGGAATCCCAGCCTCTAGAACTGTAAGAAATAAATAT  
TTGCTGTTTATAATCCAA







**FIGURE 242**

MRSCLWRCRHLSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHRQRTENIKERSLQSLAKP  
KSQAPTRARRTTIYAEPA PENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW  
KSPEKEKTMVNTLS PRGQDAGMASGRTEAQSWKSQDTKTTQNGGQTRKLTASRTVSEKHQG  
KAATTAKTLIPKSQHRMLAPTGA VSTRTRQKGVTTAVIPPEKKKPQATPPPAPFQSPTTQRN  
QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLF LPNLTLFLDSRHF  
NQSEWDRLEHFAPPFGFMELNYSLVQKVVTREFPVPQQQLLLASLPAGSLRCITCAVVGNNG  
ILNNSHMQEIDSHDYVFR LSGALIKGYEQDVGTRTSFYGF TAFSLTQSLLILGNRGFKNVP  
LGKDVRYLHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEA FREALHMDRYLLLHPDFL  
RYMKNRFLRSKTTLDGAHWRIYRPTTGALLLLTALQLCDQVSAYGFITEGHERFSDHYDYTSW  
KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

**Cytoplasmic Domain:**

amino acids 1-10

**Type II Transmembrane Domain:**

amino acids 11-35

**Lumenal catalytic Domain:**

amino acids 36-600

**Ribonucleotide Reductase small subunit Signature:**

amino acids 481-496

**N-glycosylation Sites:**

amino acids 300-303, 311-314, 331-334, 375-378, 460-463



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**FIGURE 244**

MRGPGHPLLLGLLLVLGPSPEQRVEIVPRDLRMKD KFLKHLTGPLYFSPKCSKH FHRLYHNT  
RDCTIPAYYKRCARLLTRLAVSPVC MEDK

1000  
900  
800  
700  
600  
500  
400  
300  
200  
100  
0  
-100  
-200  
-300  
-400  
-500  
-600  
-700  
-800  
-900  
-1000

**FIGURE 245**

GGGCTGGGCCCCGCCGACGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGAGG  
 CCGGACCCCGGCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCGCGCCG  
 CTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCTGGTGCTGGCCGGCGAGGACTGCCT  
 GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTTCACCTTCT  
 GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCGAGAGG  
 CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT  
 CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCCCTGTTGCTACCTGT  
 ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTTGAAGGCCAGGAGATTTCCAATGACAGGCATC  
 CCAGTGCCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC  
 TGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCAATATCCACTCTACCCAGCTGGGCCCC  
 CAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC  
TGAGGAACCAGCCATGTCTCTGCTGCCCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT  
 CCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGTCCTCCAGCCACCAGGCCCCAGACCAA  
 GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGGAACAGGAGCTGAACTAGA  
 ACTATGAGGGGTTGGGGGAGGGCTTGAATTATGGGCTATTTTTACTGGGGCAAGGGAGG  
 GAGATGACAGCCTGGGTACAGTGCCTGTTTTCAAATAGTCCCTCTGCTCCCAAGATCCCAG  
 CCAGGAAGGCTGGGGCCCTACTGTTTGTCCCCTCTGGGCTGGGGTGGGGGAGGGAGGAGGT  
 TCCGTGACGAGCTGGCAGTAGCCCTCCTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTG  
 CTAGATTAAAGCTGTAAAGACAAAA

## **FIGURE 246**

MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHRYC  
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQQLQSP  
FEGQEIPMTGIPVQPVYPYPQDPKAGFAPPQPGFMYPPSGPAPQYPLYPAGPPVYNPAAPP  
YMPPQPSYPGA

### **Transmembrane Domains:**

amino acids 10-28, 85-110

### **N-glycosylation Site:**

amino acids 38-41

### **N-myristoylation Sites:**

amino acids 5-10, 88-93



**FIGURE 248**

MVFLPLKWSLATMSFLLSSLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH  
 YDLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLQVLE  
 HPPQEQIALLAPEPLLVLGYPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA  
 ARMAFFCFDEPAFKASFSIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLV  
 FIISDFESVSKITKSGVKVSUYAVPDKINQADYALDAAVTLEFYEDYFSIPYPLPKQDLAA  
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVVAHELHQWFGNLVTMEWNNDL  
 WLNEGFAKFMEFVSVSVTHPELVKVDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD  
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMGD  
 FCSRSQHSSSSSHWHQEGVDVKTMMNTWTLQRGFPLITITVGRNVHMKQEHYMKGSDGAPD  
 TGYLWHVPLTFITSKSNMVHRFLLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL  
 TGLLKGHTAVSSNDRASLINNAFQLVLSIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIP  
 MYKLEKRDMMNEVETQFKAFLIRLLRDLIDKQTTWDEGSVSEQMLRSELLLLACVHNYQPCV  
 QRAEGYFRKWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSTESQIEFALC  
 RTQNKEKLQWLLDESFKGDKIKTQEFPPQIITLIGRNPVGYPLAWQFLRKNWNKLVQKFELGS  
 SSIAHVMVGTNNQFSTRTRLEEVKGFFSSSLKENGSQLRCVQQTIIETIEENIGWMDKNFDKIR  
 VWLQSEKLERM

**Signal peptide:**

amino acids 1-34

**N-glycosylation sites:**

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

**Neutral zinc metallopeptidases, zinc-binding region signature:**

amino acids 350-360



**FIGURE 249**

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCAC  
 TGCCAGGAGTGCAGGCGTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC  
 GACCTACCCCGGAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA  
 CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG  
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC  
 TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT  
 TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGTCTGCTTGTCTATGG  
 AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCAAGGGGACCACACACTGTTATGAT  
 GGCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCAATCTGAGAGTCCAGGGATGCATGCC  
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCGTGGGTATGACTGAGA  
 ACTGCAATAGGAAAGATTTTCTGACCTGTCAATCGGGGGACCACCATTATGACACACGGAAAC  
 TTGGCTCAAGAACCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT  
 GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAG  
 GCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGG  
 GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG  
 CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCGTGCCCAGGAGACCGGCAGTGTG  
 CTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGCGTCCCCCGAATGACCTGCCCCAGG  
 GCGGCCACTCATTGTTATGATGGGTACATTCTCTCAGGAGGTGGGCTGTCCACCAAAAT  
 GAGCATTGAGGGGTGCGTGGCCCAACCTTCCAGCTTCTTGTGTAACACACCAGACAAATCG  
 GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT  
 GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG  
 GTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTACCGCTGCTGA  
 CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGACACCAGATTCTTTC  
 CCATTCTGTCCATGAATCATCTTCCCCACACAAATCATTATCTACTACCTAACAGCA  
 AACTGGGGAGAGCCTGGAGCATCCGGAATTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG  
 GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA



**FIGURE 251**

GCGACGGGCAGGACGCCCCGTTTCGCCTAGCGCGTGCTCAGGAGTTGGTGTCCTGCCTGCGCT  
 CAGG**ATG**AGGGGGAATCTGGCCCTGGTGGCGTTCTAATCAGCCTGGCCTTCCTGTCACTGCTG  
 CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTCGTCCCTGG  
 CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGACGGCCTGGAAGAGTCG  
 GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTCGTCTAT  
 GGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC  
 TGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG  
 AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTGCGC  
 GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA  
 CGCCACGCTGTCTGCCAGGGCCGCGGGGGCACGCTGAGCATGCCCCAAGGACGAGGCTGCCA  
 ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCGTGTCTTCATCGGCATCAAC  
 GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCCATGCGGACCTTCAACAA  
 GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCT  
 CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG  
 GAGAACATG**TGA**GCCTCAGGCTGGGGCTGCCCATTTGGGGGGCCACATGTCCCTGCAGGGTT  
 GGCAGGGACAGAGCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAG  
 GCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAATGGCCTATGCTTAAGAGGAAAAATG  
 AAAGTGTTCTGGGGTGCTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA  
 ATGTCAATTATGTAATTATTATCCAGAAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGC  
 TATACAATAAAAATCTTTAAGTAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAA



**FIGURE 253**

AGTGACTGCAGCCTTCCTAGATCCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG  
CACCAGTGTGTGAGGGGAGCAGGCAGCGTCCTAGCCAGTTCCCTTGATCCTGCCAGACCACC  
CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCA**ATG**AGGATCATGCTGCTATTACAGCCAT  
CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG  
TTCTGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC  
AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA  
GGAATCAACATCTCCCAGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA  
GGAGCGTCCAGCCAGAGGGAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCCTCGGCCC  
CTTCATCCCAATCAGCTTGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC  
TTT**TAAG**ACTCTCCTACGGATGTGAATCAAGAGAACGTCCCAGCTTTGGCATCCTCAAGT  
ATCCCCGAGAGCAGAATAGGTACTCCACTCCGGACTCCTGGACTGCATTAGGAAGACCTC  
TTTCCCTGTCCCAATCCCAGGTGCGCACGCTCCTGTTACCCTTTCTCTTCCCTGTTCTTGT  
AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAAACTGCA  
TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCTGTAGTGT  
CCTACATTAATAAATATAATGTCTCTCTATTCCTCAACAATAAAGGATTTTGCATATGAA  
AA

## **FIGURE 254**

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK  
ALSQASTDPKESTSPKRDMDHDFVGLMGKRSVQPEGKTGPFLLPSVRVPRPLHPNQLGSTGK  
SSLGTTEEQRPL

**Important features:**

**Signal peptide:**

amino acids 1-18

**Tyrosine kinase phosphorylation site.**

amino acids 36-45

**N-myristoylation site.**

amino acids 33-39, 59-65

**Amidation site.**

amino acids 90-94

**Leucine zipper pattern.**

amino acids 43-65

**Tachykinin family signature.**

amino acids 86-92



## **FIGURE 256**

MSCVLGGV IPLGLLFLVCGSQGYLLPNVTLLLEELLSKYQHNEHSRVRRAIPREDKEEILML  
HNKLRGQVQPQASNMEYMSAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGR  
GGSRLCSVLFVCFETGSHSATDAGVQWHNRHALKP

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **N-glycosylation site.**

amino acids 27-31, 41-45

#### **N-myristoylation site.**

amino acids 126-132, 140-146

#### **Amidation site.**

amino acids 85-89



**FIGURE 257**

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**ATG**GG  
GTCTGGGCTGCCCCCTGTCCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGG  
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCCTATGAGTCCAGC  
TTCCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC  
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA**TGA**CAGCCATTGAAGCCTG  
TGTCTTCTTGCCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTT  
CAGCAGGCCCCACCTCCTGAGTGGCAATAAATAAAATTCGGTATGCTG

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**FIGURE 258**

MGSGLPVLVLLTLLGSSHGTGPGMTLQLKLKESFLTNSSESSFLELLEKLCLLLHLPSGTS  
VTLHHARSQHHVVCNT

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**FIGURE 259**

AATTGTATCTGTGTAATGTTAAACAAACGAAATAAAATAGAAGGAAAACTTTCTGAGTTT  
CAAAAACAACAGACTAGTACTCTAAAGAACTCTTTAAACAATTAAGTGTAGGATTGCAGT  
**TATG**ATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC  
TATTAATATTTACCATTGCAGAAGCTTCATTCAAGTGTGAAATGAATGCTTAGTGGATCTG  
TGCCCTTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTCCCCCTCC  
CTCCGATTGTTCTAAAT**TAA**TTGAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAAATCTG  
TATGATTCTCAACCATCTTTAGTTGGGAAAGTCCCTGAAAGCCAATGGAATACTTTTTTTT  
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA  
GTAAATAGAAACCTGTGTTTATTCTCAGGTATTTAGAAACAACAGCCATCATTTTATTTT  
ATGTGTGTGTTCTTGGCTGTATTCTATAAATTATATATTTTGGGCTATCAAATATTACTTCAT  
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTTGCATTTTCTC  
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTACTA  
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGAATTGATATTAATAAAACCAGA  
ATAAAAGTTCATATCTACCC

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## **FIGURE 260**

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLP  
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GAGGATTTCGCCACAGCGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTTGAGAAGGCCACGACATAGAGACTGCGCTTGCTGGTGTTTGCGAGGATGATGGTGCCTTCGAGAGCTTCTGCATTGCTGTTCTGTTCTTGACGTTTCTGCCCCGCCGACGCTATCCAGAGCACCACCCATGGTGCTATTACATCTACCAGCGCTTCTCGAGTCTTGGAGCAGGGCTGGAAAAATGTACCCAAAGCAGGAGGCTATACATCAAGAATTCGAAGTTCTCAAAAATATACTGTCTCATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAACCTGGCATCGAGAGTTGAACCTGCCCAACGGGAGATTGACTACATACAACTCATCTCGAGAGGCTACAGAGTGCACTCGTATCAGAGGACAGACATCGGACAAGATGTTGCTCCAAGAAGTGAAGAAAGAAAAGATCCGGAGCTGCTGTAATGCAGGCTGTGACAACATGCTGATGGGACATAAGCTTTTGAATAATGTGAAGAAGATGTGAGCACACATGGCTCTGGATGAAGAAGTCTGTCTATAACTCTCCAAGGTTGACTTATTAATTTGGATCCAGAAACAACTGTTTGGGAATTTGCAAAACATACCGGCTATTCATGGAGGATAACACCAAGCCAGCTCCCCGGAAAGCAATCTTAACACTTTCTGGCAGGGAAGACGGCCAAGTGATCTACAAAGGTTTTCTATTTTTCATTAACAGCAACTCTAATGTAGATAAATCAAAATATAACCTGCGACAAGAGAGCTGTGGAAGATCGAATGCTGCTCCCAAGGAGGTGAGGCCAGCATTTGGTTTACCAGCATCCCCCTCAACTTACATTGACTGGCTGTGGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCACCCATAGCCATTTGGTTCTCACAAAGATTGAGCCGGGACAGCTGGGAGTGAGCATTCATGGGATACCCCATGCAAGAACGGGATGCTGTAAGCCTCATCTCTTGTGTGGGTTCTCTATGTGGTCTACAGTACTGGGGGCCAGGGCCCTCATCTGCATACCTGCATATGATATGCCATGGGCACATTCAGTGAGGAGGACTTGC CCAACTTGTCTTCTCCCAAGGACCAATAGATCTACTCCTATGATCATTACAACCCAGAGAT AAGCAGCTCTATGCCCTGGAATGAAGGAAACCAGATCATTTACAACTCCAGACAAAGAGAAA GCTGCTCTGGAAGTAAATGCATATACAGTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTC TACAGGACAGTAGGAGCTATAGCCCTTACAATATAGTATCCCTCAATACACACAGGAAG AGTGTTGAGAAGTGGAATACGTATGCCCTCTTCCCAATGTCACTGCTTATAGGTATCTTC CAAGAGCTTAGATGAGAGCATATCATCAGGAAAGTTTACAACATGCTCCATTACTCCCCCAA CCTCTGGCTCTCAAGGATGACCACATTCTGATACAGCCTACTTCAGGCCTTTTGTTTTACT GCTCCCCAGCATTTACTGTAACTCTGCATCTCCCTCCCACAATTAGAGTTGATAGCCAGC CCTTAATATTCACCATGGCTTTCTCTCCCTGGCCTTTGCTGAAGCTCTTCCCTCTTTT CAAATGTCATGTGATATTTCTCCCATTTTCACTGCCCAACTAAATACTATTAATTTCTTT CTCTTCTTTTCTTTTGTGACAAAGGCTCCTATGTTGGCCAGGCTGGTCTCAAACCTC AGAGCTCAAGAGATCCTCTGCTCAGCCTCCTAAGTACTGGGATTACAGGCATGTGCCAC CACACTGGCTTAAATATCATTTTCTATTGAGGTTTAACTCTATTCTCCCTAGCCCTGTC CTCCACTAAGCTTGGTAGATGTAATAAAGTGAATAATTAACATTGAAATCGCTT CCAGGCTGGAGGTGTTTGCACATCATTTGAATCTCGTTTACCTTTGTGAACATGCAAGAG TCTTTACAGCTGTCACTTGAGTTTGTAGTGAGTAAACAACATTAACAAGTGAAGAATACAGC TAGAAAATACTACAAATCCCATAGTTTTCATTTGCCCAAGGAAGCATCAAATACGTATGTT TGTTCACCTACTCTTATAGTCAATCGCTTCATCGTTTCAGCCTAAAAATATAGTCTGCC TTAGCCAGTTTTCATGCTGCACAAGACCTTCAATAGGCCTTCAAATGATAATTCTCTC AGAAAACCAAGCTCAAGGTTGAGGACCCCACTCTAGCCTCTCTGTCTGTCTGCTCTCTGT TTCTCTCTTCTGCTTTTAAATCAATAAAGTGACACTGAGCAAAAAA

**FIGURE 262**

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FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQRIDYIQYLREADECIVSEDKTLAEMLL  
QEAEEEKKIRTLNASC DNMLMGIKSLKIVKKMDTHGSMKDAVYNSPKVYLLIGSRNNTV  
WEFANIRAFMEDNTKPAPRKQILTLWQGTGQVIYKGFLFFHNQATSNEIIKYNLQKRTVED  
RMLLPGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPGTLGVEHSWDT  
PCRSQDAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIH  
YNPRDKQLYAWNENQIIYKLQTKRKLPLK

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GGGGCCCGCGGTACTCACTAGCTAGGTTGGCAGTGGTTCCACCAAC**ATGG**AGGCTCTCGCAGA  
TGTCGGAGGACTCATGGGGCTGTGCGGTGTGTTGGGCTGCTGGCCCTGATGGCAGCGCGCGG  
GTAGCGCGGGGGTGCTGCGCGCGGGGGAGGAGAGCGCGCGCGCTGCCAAAAAGC  
AAATGGATTTCACCTGACAAATCTTCGGGATCCAAGAAGCAGAAACAATATCAGCGGATTC  
GGAAGGAGAAGCTCAACACACAACTTCAACCACCGCTCCTGGCTGCAGCTCTGAAGAGC  
CACAGCGGAACAATATCTTGCATGGACTTTAGCAGCAATGGCAAAATACCTGGCTACCTGTGC  
AGATGATCGCACCATCCGCATCTGGAGCACCAGGACTTCCTGCAGCGAGAGCACCAGCAGC  
TTAGACGCAACCGTGAGCTGGACACGCCACCCCTGTGCGCTTGACGCCCTGACTGCAGAGCC  
TGACTCGTCTGGCTGGCCAACGGGTAACCTCGTGTCTTCAAGATGACCAACAGATGAACAACAC  
TGGGGGCTACACCTTCACAGCCACCCAGAGGACTTCCTAAAAAGCACAAGGCGCTGTCA  
TCGACATTTGGCATTTGCTAACACAGGGAAGTTTATCATGACTGCCCTCCAGTGACACCATGTC  
CTCATCTGGAGGCTGAAGGTTCAAGTGTCTGTACCATCAACCAACAGATGAACAACAC  
ACACGCTGCTGTATCTCCCTGTGGCAGATTTTGTAGCCTCGTGTGGCTTCACCCCAGATGTGA  
AGGTTTGGGAAGTCTGCTTTGAAAGAAAGGGGAGATTCAGGAGGTGTGTCGAGCGCTTCGAA  
CTAAAGGCGCTACCGCGCTGTGCATCGTTTGTCTTCAACAGCATCACGAGAGATGGC  
TTCTGTCTCCAAGGATGGTACATGGAAACTGTGGGACACAGATGGGAATCAAGAGAAGAGC  
AGGAGCCCTTACTTCTGAAGACAGGCGCTTTGAAGAGGCGGCGGGTCCGCGCGCTGCGGC  
CTGGCCCCCTCCCCAACGCCAGGCTTTGGCTTTGGCCAGTGGCAGTAGTATTCATCTTA  
AAATACCGCGCGGGCGAGAAGGAGGAGTGCTTTGAGCGGGTCACTGGCGAGGTGATCGCCA  
ACTTGTCTTTGACATCACTGGCGCTTTCTGTGCCCTCTGTGGGACCGGGCGGTGCGGCTG  
TTTCAACAACACTCTGGCCACCGGACCATGGTGGAGGAGATGCAGGGCCCACTGAAGCGGGC  
CTCAACAGAGAGACCGGCCAGAGGCTGCAGCAGAGTGAACCGAGGCCCAAGAGACCTGA  
AGAGCTTGGGTGCCCTGAAGAAG**TG**ACTCTGGGAGAGGCCCGCGCGCAGAGGATTTGAGGAGGAG  
GGATCTGGCGCTTCATGGCACTGCTGCCATTTTCTCCGAGGTGGAAGGCTTTCAAGAAG  
AGTCTCTCGTTTTCTTACTGTGGCGCTGCTTCTTCCATTGAACTACTCTTGTCTACTT  
AGGTTCTCTCTCTTCTGTGCTGGCTGTGACTCTCTCCCTGACTAGTGGCCAAAGCTCTTTCTTC  
CTCCAGCGCCCACTGGGTGGAATTCTGTCCCACTGGCACTGAGGAGAAATGGTAGAGGAGG  
AGGAGAGAGAGAGAGAAATGTGATTTTGGCCCTGTGGCAGCATCTCTACACCCAAAGAG  
TTTGTAAATGTTCCAGAACCACTGAGAACACCTGAGTACTAGACGACGATTTTGCAGGA  
TGGGAGACTGGGATGACTTCCCATCAAGAACTGTGTTTCATCAAAAGGACACTAAGGGATT  
TCCTTCTGGGCTCAGTCTATTGTGTAAGATGAGAAATATCTCTGTGACTACTCTTGCA  
AAGATGATATGAGGCTAAGAGAATATCAAGTCCCAGTCTGGAAGAAAAGTAGAAAAAGT  
AGTACTATTGTCCAATGTCAATGAAAGGGTAAAGGGGGAACCGATGTGCTTTGAAACCAAA  
TTAGAAACACATCTCTTGGGAAGGCAAGTTTCTGGGACTGATCATACATTTTATATGGT  
TGGGACTTCTCTCTTGGGAGATGATATCTTGTTTAAGGAGACCTCTTTTCAGTTTCATCAAG  
TTGACTCAGATATTGAGTGCCCACTCTGTGCCAAATTAATATGAGCTGGGATTAAAAAA  
AAAAA

**FIGURE 264**

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQK  
QYQIRKEKPQQHNFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ  
REHRSMRANVELDHATLVRFSPDCRAFIVWLANGDTLRVFKMTKREDGGYTFATPEDFPKK  
HKAPVIDIGIANTGKFIMTASSDTTVLIWSLKGQVLSTINTNQMNTHAAVSPCGRFVASCG  
FTPDKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV  
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH  
GECIANLSFDITGRFLASCGDRAVRLFHNTFPGHRAMVEEMQGHCLKRASNESTRQRLQQQLTQ  
AQETLKS LGALKK

**Important features:****Signal peptide:**

amino acids 1-25

**N-glycosylation site.**

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

**Beta-transducin family Trp-Asp repeat protein.**

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308



**FIGURE 265**

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG  
CAGTGTTTTGCCCTTACCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCC  
TCCTAGTAACGTGTGCTGACTGTGCTGTGATCACAGGGGCTGTGAGCGGGATGTCCAGTGT  
GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCAACCCGCT  
GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCCTTCTTCAGGAAACGCA  
AGCACACACCTGTCTTGTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTAC  
CGCTGCTCCATGGAATTGAAGAACATCAATTTTTAGGCCTTGCTGGTCTCAGGATACCCA  
CCATCCTTTTCTGAGCACAGCTGGATTTTATTCTGCCATGAAACCCAGCTCCCATGAC  
TCTCCAGTCCCTACACTGACTACCCTGATCTCTCTTGTCTAGTACGCACATATGCACACAG  
GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTACAGCTTGAGG  
CTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTCTTCCCCTGCTCAGGCTGCCAGAGAGGTGGTA  
AATGGCAGAAAGGACATCCCCCTCCCCTCCCAGGTGACCTGCTCTCTTCTTCTGGGCCCTG  
CCCCTCTCCCACATGTATCCCCTCGGTCTGAATTAGACATTCTCGGGCACAGGCTCTTGGGT  
GCATTGCTCAGAGTCCCAGGTCTTGGCCTGACCCTCAGGCCCTTACAGTGAAGTCTGTGAGG  
ACCAATTTGTGGGTAGTTTATCTTCCCCTGATTGGTTAACTCCTTAGTTTTCAGACCACAGAC  
TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTACCCCAAGGCAGGTGTAGGGAGCCCA  
GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTGTGGCCTGTGA  
CCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGCCCCCTCTTACCACACTTTACCAGT  
TAACCACTGAAGCCCCCAATTCCACAGCTTTTCCATTAAATGCAAAATGGTGGTGGTTCAA  
TCTAATCTGATATTGACATATTAGAAGCAATTAGGGTGTTTCTTAAACAACTCCTTTCCA  
AGGATCAGCCCTGAGAGCAGGTTGGTGACTTTGAGGAGGGCAGTCTCTGTCCAGATTGGGG  
TGGGAGCAAGGGACAGGGAGCAGGGCAGGGGCTGAAAGGGGCACTGATTGAGACCAGGGAGG  
CAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCACACTGAAAAA

## **FIGURE 266**

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEETCHP  
GSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

**Signal peptide:**

amino acids 1-19

**Tyrosine kinase phosphorylation site:**

amino acids 88-95

**N-myristoylation sites:**

amino acids 33-39, 35-41, 46-52





**FIGURE 268**

MSFLQDPSFFTGMWSIGAGALGAALALLLANTDVFLSKPQKALEYLEDIDLKTLEKEPR  
TFKAKELWEKNGAVIMAVRRPGCFLCREEADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF  
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWVYNFFRAWNGGFSGNLEGEFGFILGGVFV  
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

MSFLQDPSFFTGMWSIGAGALGAALALLLANTDVFLSKPQKALEYLEDIDLKTLEKEPR  
TFKAKELWEKNGAVIMAVRRPGCFLCREEADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF  
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWVYNFFRAWNGGFSGNLEGEFGFILGGVFV  
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

**FIGURE 269**

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCG  
GGCCAGGTGCCCCGTGCGAGGTGCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA  
AGCCCCCTTCCTCGGCGCTGCCAACCCGCCACCCAGCCCC**ATG**GCGAACCCCGGGCTGGGGCTG  
CTTCTGGCGCTGGGCCTGCCGTTCTGTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA  
GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG  
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGCTGCCTTG  
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG  
CACCTACCGGCCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG  
ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCCATC**TAG**GTCCCTCTCCTGCATCTGTCTCC  
CTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG  
TGCTTAATAGCAGGAAGAAGGTACTTCAAAGACTCTGCCCTGAGGTCAAGAGAGGATGGG  
GCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

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**FIGURE 270**

MANPGLGLLLALGLPFLARWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIV  
VFSLLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

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**FIGURE 271**

AATATATCATCTATTTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGTT  
TTGGGATTTTAATTTTCAAACACAGCAGAATGACATTTTCTGTCACTATTATTATTGTTG  
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT  
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC  
CTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA  
GGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG  
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA  
TATACAATAAGGTGAAATTATAAGTACCCATATGCAGTTGGCTGGACAGTTCCTAAATTGGACT  
TTATTAATTTTAAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA  
TCATATAATTTGATACAAATAAAAGAAAAGTGTTCTCTCCCTTACAGAATTGACATTTTAA  
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA  
AGAAGGGAAAATGTTGCCAAGGAAAAAAAAA

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**FIGURE 272**

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK  
GIVKGRNLDSRGLILGAEAWGRGVKKNT

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**FIGURE 274**

MGLFRGFVFLVLCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIIIEQIEDMVTTASTY  
 LFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKKHADVIVAPPTLPGRDEPYTKQFTEC  
 GEKGEYIHFTPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQFFYRAKSKKIEATR  
 CSAGISGRNRVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDKVQTEKASIMFMQSIDSVVE  
 FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDfKNTIPMVTPPPPPVFSLLKISQRIVCLV  
 LDKSGSMGKDRNLNRMNQAAKHFLLOTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLM  
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLTGDGEDNTASSCIDEVKQSGAIVH  
 FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT  
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSTIMENFTVDATSKMAYLSIPG  
 TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPI TVNAKMNDVNSFPSPMIVYAEILQG  
 YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDDGVYSRYFTAYTENGRYSLKVRAGH  
 GANTARLKLRPPLNRAAYIPGWVNGEIEANPPRPEIDEDTQTTLDFSRASGGAFVVSQV  
 PSLPLPDQYPPSQITDLATVHEDKIIILTWTAPGDNFDVGKVQRYIIRISASILDLRDSFDD  
 ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIQVTLFIP  
 QANPDDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

**Signal peptide:**

amino acids 1-21

**Putative transmembrane domains:**

amino acids 284-300, 617-633

**Leucine zipper pattern.**

amino acids 469-491, 476-498

**N-glycosylation site.**

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,  
628-632, 811-815, 832-836, 837-841, 852-856, 896-900



**FIGURE 276**

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQALALPRANSPTGKEGYQAVLQ  
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL  
HSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVKDKRDELVEAIES  
ALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSP  
MKVKNEKLNMAANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK  
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR  
LNTQPGKKVFYPVLFQYNPGIYYGHDAVPPLEQQLVIKKETGFWRDFGFGMTQCQYRSDFI  
NIGGFDLDIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKRCMDELTPQYKMCMQS  
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

**FIGURE 277**

GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTATGCTGAACTCTGTCAACC  
 AGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT  
 ATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA  
 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGT  
 ATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCTGCTGTTGAGGTGC  
 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACT  
 CTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG  
 GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT  
 CAGGGATCTGGCAACGTAGAAGAAAGAACAAGAACCATCTGAAGTGGATGACGCTGAAGAT  
 AAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGG  
 GGGCATATTAATGATGCCTTCTGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT  
 TGTTCTGCTTCCTCAAGAAATTAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATA  
 CCAAGAGCAGATCATATATTTGTTTCACCATTCTTCTTTTGAATAAATTTGAATGTGCT  
 TGAAAGTGAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGAC  
 TCAAAATATTCTAAATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG  
 TAGTTATTGATTTAAGCATTTTTAGAAATAAGATCAGGCATATGTATATATTTTCACACTTC  
 AAAGACCTAAGGAAAAATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT  
 TGAAAAATGGATCCTTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG  
 TGAGAAGTAATTATTGTAAATGGATGGATAAAAAATGGAATTACTCATATACAGGGTGAATT  
 TTATCCTGTTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGAC  
 AATTCTATTTGTTGACCATTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAG  
 TAATAATCATCTCTTTTTAAAAAAAAAAAAAAAAAAAAAAAAA



**FIGURE 279**

AACTCAAACCTCTCTCTGCGAAACGCGGTGCTTGCTCCTCCCGAGTGGCCTTGGCAGG  
 GTGTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAAGCTGGGTTCCTC**ATGT**  
 ATGGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGG  
 CCTATAGCAGCTGTGGAAATTTATACCTCCCGGGTGTGGAGGCTGTTAATGGGACAGATGC  
 TCGGTTAAATGCACTTTCTCCAGCTTTGCCCCGTGGGGTGATGCTCTAACAGTGACCTGGA  
 ATTTTCGTCTCTAGACGGGGGACCTGAGCAGTTTGTTATTCTACTACCACATAGATCCCTTC  
 CAACCCATGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGA  
 TGCCTCCATCCTTCTCTGGAACCTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA  
 AGAACCCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA  
 CGCTTCTCTGAGATCCACTTCCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT  
 AATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC  
 ATAAAGTGGTGGAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT  
 GTTTATTTAGAAGACACAGACT**TAA**CAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACA  
 GAACCCTAGTATTTCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT  
 TTTCCAACCAAGTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC  
 AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTCAGA  
 GTGTAAATTTTTCAAGTGCTCATTAGGTTTTATAAACAAGAAGCTACATTTTGGCCCTTAA  
 GACACTACTTACAGTGTATGACTTGATACACATATATTGGTATCAAAGGGGATAAAAGCC  
 AATTGTCTGTTACATTTCTTTTACGTATTCTTTTAGCAGCACTCTGTCTACTAAAGTTA  
 ATGTGTTTACTCTCTTTCCCTTCCACATTCTCAATTAAAGGTGAGCTAAGCCTCCTCGGTG  
 TTTCTGATTAACAGTAAATCCTAAATTCAAACTGTTAAATGACATTTTATTTTATGTCTC  
 TCCTTAACATATGAGACACATCTTGTTTTACTGAATTTCTTTCAATATTCCAGGTGATAGATT  
 TTTGTCG

**FIGURE 280**

MYGKSSTRAVLLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT  
WNFRPLDGGPEQFVFYYHIDPFQPMSEGRFKDRVSWDGNPERYDASILWKLQFDDNGTYTCQ  
VKNPPDVGVIIEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVIVVVLFQHYRKKRWAER  
AHKVVEIKSKEERLNQEKKVSYLEDTD

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**FIGURE 283**

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCAAGGAAGTGGTTCCAACCTTGGACCC  
CTAGGGGTCTGGATTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGA**ATGC**  
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTACGGTGGCCTGGTCCCTCCTTGCCGAGAGA  
GTGTCTGGGTCAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC  
ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG  
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGCCAGTCCAGGGTGGGGGGCG  
GCAAACTCCATAAAGAACCAGAGGGTCTGGGCCCGGCCACAGAGTCATCTGCCAGCTCCT  
CTGCTGCTGGCCAGTGGGAGTGGCACGAGTGGGGCTTTGTGCCAG**TAA**AACCACAGGCTGG  
ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA  
CCCCAAAGAGCTTTCATTGTATCTATTGATTTTACCACATTAGCAATTAAACTGAGAAAT  
GGGCCGGGCACGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT  
CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGCTACTAAAAA  
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCCAGTTACTCGGAGGCTGAG  
GCAGGAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT  
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA



**FIGURE 285**

GTCATGCCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA  
GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCCTGCTCTTCCATGG  
GACCCTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA  
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTCAGC  
CGGGGCCGGGATGCAGCCCAGGAActTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA  
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCCAGGCACAGA  
AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT  
GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC  
CCTCACAGGCCACGTGCAGCGGCAGAGGCGGAGATGGTGGCACAGCAGCATCGGCTGCGAC  
AGATCCAGGAGAGACTCCACACAGCGGCGTCCAGCCTGAATCTGCCTGGATGGAActGAG  
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG  
CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC  
GCAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA  
CCCTTTCATGCCTACACACCCCTCATTAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 286**

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLLFHGTLQLGQALNGVYRTTEGRLTK  
ARNSLGLYGRTIELLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK  
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAQQHRLRQ  
IQERLHTAALPA

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MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLLFHGTLQLGQALNGVYRTTEGRLTK  
ARNSLGLYGRTIELLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK  
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAQQHRLRQ  
IQERLHTAALPA









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**FIGURE 290**

MKLAALLGLCVALSCSSAAAFVLGSAKPVAQPVAALESAAEAGAGTLANPLGTINPLKLLLS  
SLGIPVNHLEGSQKCV AELGPQAVGAVKALKALLGALT VFG

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**FIGURE 292**

MKVVP S L L L S V L L A Q V L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E  
E E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I  
K R G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F  
D T E C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P  
V F T E V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L  
A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A  
T G R N L Q V S R V L R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F  
L G R V V N P T L L



**FIGURE 294**

MRRLLLVTSLVVLLWEAGAVPAPKVPIKMQVKhWPSEQDPEKAWGARVVEPPEKDDQLVVL  
FPVQKPKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHFPPEEDQGEE  
RPRLWVMPNHQVLLGFEEQQDHIYHPQ



**FIGURE 295**

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGAGGGAGGGAGTGAAGGAGCTCTCTG  
 TACCCAAGGAAAGTGACAGCTGAGACTCAGACAAGATTACA**ATGA**ACCAACTCAGCTTCCTGC  
 TGTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA  
 TGGACCTGTTCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC  
 TAGTGCAATTTGATGGCCTGTATTTCTCCGCACTGAGAATGGTGTTATCTACCAGACCTTCT  
 GTGACATGACCTCTGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATG  
 CGTGGGAAGTGACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC  
 AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG  
 ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG  
 CCCAATAAGTCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC  
 TGGCTTCCTCCAGCACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT  
 ATGGAGAAGGAAAGTGTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGC  
 GACGCCCAGAAAACAGCATCTTATTACTCACCTATGGCCAGCGGGAATTCAGTGCGGGATT  
 TGTTCAAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAACGCCTTGTGTGCTGGAATGAGGG  
 TCACCGGATGTAACACTGAGCATCACTGCATTTGGTGGAGGAGGATACTTTCAGAGGCCAGT  
 CCCCAGCAGTGTGGAGATTTTCTGGTTTGGATTGGAGTGGATATGGAAGTCACTGTTGGTTA  
 CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGT**TGA**GAGTTTTGTG  
 GGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCAAGGATGGAGAACAACCTTACCCA  
 GTAGCTAGAAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGAAAAAA

**FIGURE 296**

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN  
GVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDWSSQQGSKADYPEGDGNWANYNTFG  
SAEAATSDDYKNPGYYDIQAKDLGIWHVFNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI  
YQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYYSPIYQREFTAGFVQFRVFNNERAAN  
ALCAGMRVTGCNTEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSSREITEAAVLL  
FYR

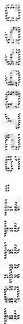


**FIGURE 297**

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC  
 CACGAGGCTGCCGCATCCTGCCCTCGGAACAATGGGACTCGGCGCGGAGGTGCTTGGGCCG  
 CGTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCCATGAAAGCGCAGCC  
 ATGGCGGCATCTGCAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC  
 AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAACTTCCAACAGTACTGTGAAAC  
 CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG  
 GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC  
 TACACCCAAAAACAACAAGTGTTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG  
 TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACATATGCAT  
 TCTGAAGCAAAGAAAGGATCAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAC  
 GCTGGGAGTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTC  
 GGTATCGAACCATAGATGAACATGATGCCATCATTTAAGGAATCCATGGACCAAGGATGGA  
 ATACAGATTGATGCTGCCCTATCAATTAATTTGGTTTATTAATAGTTTAAACAATATTCT  
 CTTTTTGAAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA  
 AAGATTCTTCAAGGTAACAAGGGTTTGGGTTTGAATAAACATCTGGATCTTATAGACCGT  
 TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTTTTTTGGCT  
 GGGGTGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAA  
 TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGT  
 AGCTCACATAAAGAACTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA  
 CAGAAATTATACAATCAAACCTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTG  
 TGCTTTAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

**FIGURE 298**

MGLGARGAWAALLLGT LQVLALLGAAHESAAMAASANIENSG LPHNSSANSTETLQHVP SDH  
TNETSNSTVKPPTS VASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQN  
TSQISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIG  
CKMYYSRRGIRYRTIDEHDAII



**FIGURE 299**

CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGG  
 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCG**ATG**GCGACCCTGTGGGGAGGC  
 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTGCTGCTGGCGCTTTCGGTGTCTGTCTGGC  
 GCAGCTGTGACAGCCGCCAAGAATTTGAGGATGTGAGATGTAAATGTATCTGCCCTCCCT  
 ATAAAGAAAATTTGCGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCCTT  
 CATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA  
 ATGCAAATATGAAGAAAGAAGCTCTGTCAACAATCAAGGTTACCATTATAATTTATCTCTCCA  
 TTTTGGGCCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG  
 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACACAGCCTTT  
 TGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAG  
 AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGG  
 CATGTTGTCTCTCAGC**TAA**TTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAA  
 CTGGAAGAAGTACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTGATTTACCAACT  
 GTTGTGGAAGATTCAAACTGGAAGCAAAACTTGCTTGATTTTTTTTTCTTGTAAACGTA  
 ATAATAGAGACATTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTATTG  
 TGACTTTTACTAATAAAAAATAAATCTGCCTGTAAATATCTTGAAGTCCTTTACCTGGAACA  
 AGCACTCTCTTTTTACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTTG  
 TTGTTGTTGTTTTTGTGTTGTTGTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGTT  
 AACAACTTTTTTCAAGTCACTTACTAAACAAACTTTTGTAATAGACCTTACCTTCTATTT  
 TCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTG  
 ACTTTTGCAGTGACTGATTATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGAT  
 CTAAATGCCTGGTGGCTTTTCACAAAAGCAGATTTCTTCATGTACTGTGATGTCTGATG  
 CAATGCATCCTAGAACAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG  
 GTGTGTGTTGTTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT  
 TGCAATAAAGAAATTTTATTTTAAACCAAGCCTCCCTGGATTGATAATATATACACATTTG  
 TCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACT  
 AGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTTATGGATAACTGGCTTTTT  
 TCTTCTATGTCCTCTTGGAAATGTAAACAATAAAAAATAATTTTGAACATCAA

300/330

**FIGURE 300**

MATLWGGLRLGSLLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENS<sup>1</sup>GH<sup>2</sup>IYNKNIS<sup>3</sup>  
QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERS<sup>4</sup>SVTIKVTII<sup>5</sup>IYLSILG<sup>6</sup>LLLLY<sup>7</sup>MVY<sup>8</sup>LT<sup>9</sup>L<sup>10</sup>  
VEPILKRRLFGHAQLIQS<sup>11</sup>DDDIGDHQPFANAHDV<sup>12</sup>LARS<sup>13</sup>SRANVLN<sup>14</sup>KVEYAQQ<sup>15</sup>RWKLQ<sup>16</sup>VQE<sup>17</sup>Q<sup>18</sup>  
RKSVFDRHV<sup>19</sup>VLS<sup>20</sup>

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50  
40  
30  
20  
10  
0  
10  
20  
30  
40  
50  
60

**FIGURE 301**

GCACCTGCGACCACCGTGAGCAGTCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT  
CTGGGCTTGTCTTGCTCTGTGCTGCTGCCAAGGCCTTCCTGTCCCGCGGGAAGCGG  
CAGGAGCCGCCGCCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCA  
CCAGGCACCCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG  
CATTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAAGAGGTCTG  
ATGGGGCAGATTATTCCAATCTACGGTTTTTGGGATTTTTTATATATACTGTACATTCTATT  
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATTGAAAATCTAATATGGCGATAAAAA  
TCATTGTCTACATTAAACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA  
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCACTTTCACATAAGAATG  
TTTACTCAATGTTTAAGTGTTTTGCCCAAATTCACAATAACAAGGCAGAACTAGGACTT  
GAACATGGATCTTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

**FIGURE 302**

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPTPEGKLGRFPPMMHHHQAPSDGQT  
PGARFQ~~R~~SHLAEAFKAKGSGGGAGGGSGRGLMGQIIPIYGF~~G~~IFLYILYILFKVSRIILI  
ILHQ

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800  
700  
600  
500  
400  
300  
200  
100  
0  
1000  
900  
800  
700  
600  
500  
400  
300  
200  
100  
0

**FIGURE 303**

CGGCTCGAGTGCAGCTGTGGGAGATTTTCAGTGCATTGCCCTCCCCGGGTGCTCTTCATCTT  
 GGATTTGAAAGTTGAGAGCAGCATGTTTTGCCACTGAAACTCATCTGCTGCCAGTGTTAC  
 TGGATTATTCCTTGGGCCCTGAATGACTTGAATGTTTCCCCGCTGAGCTAACAGTCCATGTG  
 GGTGATTACAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGAT  
 AGACTGGACTCTGTACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA  
 ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGGGACATCTTATGC  
 AATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA  
 AATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAG  
 AGGAGCCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTAGATGGGATGTGTTTTCCAG  
 AGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA  
 GGAGATTGTATTTTCGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGG  
 GCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATTTCCGCAATGACGGTCCATCATG  
 CTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCT  
 GGTGTTCAAGAAAACCATTGTGCTGCATGTCAGCCCGGAAGAGCCTCGAACACTGGTGACCC  
 CGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTC  
 TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAA  
 GAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACCGAAGAAGACTAATCCAGAGATAAAAG  
 AAAAACCTGCCATTTTGAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTA  
 CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCA  
 CCCAGTTTGGCCTTCTCTGAGGTGAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGGG  
 GAATGCCAAAAACACAGCAAGCCTTTTGAGAGAAGAATGGAGAGTCCCTTCATCTCAGCAGCGG  
 TGGAGACTCTCTCCTGTGTGTGTCCTGGGCACTCTACCAGTGATTTCAGACTCCCGCTCTC  
 CCAGCTGTCTCCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG  
 CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC  
 CTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAAACCCCCGTT  
 GGATCAGACCCTCCTGTGGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATA  
 AAAACCAACCCAAATCAA

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**FIGURE 304**

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPG  
EHAKDEYVLYYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYYICEIRLKGES  
QVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY  
HKLRSVEYSQSWGHFQNRVNLVGDI FRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIV  
LHVSPEEPRTLVT PAALRPLVLGGNQLV IIVGIVCATILLPVLLILIVKKT CGNKSSVNSTV  
LVKNTKKTNP EIKEK PCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWPSLR  
SDRNN SLEKKSGGMPKTQQAF

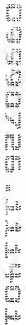


**FIGURE 305**

CTATGAAGAAGCTTCCTGGAAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATG  
GTTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG  
AAACTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCC**ATG**CA  
GGATGAAGATGGATACATCACCTTAAATATTTAACTCGGAAACCAGCTCTCGTCTCCGTTG  
GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG  
ATGGTTGTCGGGCTGGTGGCTCTGGGGATTTGGTCTGTCATGCAGCGCAATTACCTACAAGA  
TGAGAATGAAAATCGCACAGGAACCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG  
TAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCCTGTGACACAAAC  
TGGAGATATTATGGAGATAGCTGCTATGGGTTCCTCAGGCACAACCTAACATGGGAAGAGAG  
TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG  
AGTACATCAAAGCCAGGACTCATTTAATTCGTGGGTGGATTATCTCGCCAGAAGTCGAAT  
GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGGAAGA  
TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCTACCTTCTGTG  
AGAACAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT  
**TAA**TGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATGTACAATAAAAGATATGT  
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAAA

**FIGURE 306**

MQDEDGYITLNIKTRKPALVSVGPASSSWWRVMAIILLILCVGMVVGLVALGIWSVMQRNYL  
QDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSYGFRRHNLWE  
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEEFL  
EDGKGNMNCAYFHNGKMHPTFCENKHLYLMCERKAGMTKVDQLP



**FIGURE 307**

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCGCGATCCCGG  
CCCCGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCGC  
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGGGAGAA  
GCCCCGGGCAAAACGAGGCTAAGGAGACCAAAGCGGGCAAGTCGCGAGACAGCGGACAAGCAG  
CGGAGGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGG  
CGTCGTGGCC**CATG**CGGCGGCTATCGCCAGCTCGTCTCATCCGTGAGAAGAGGCAAGCCCGCG  
AGCGCGAGAAAATCCAACGCCTGCAAGTGTGTGTCAGCAGCCCCAGCAAGGCAAGACCAGCTGC  
GACAAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG  
AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC  
ACTTGCAGCTGCAGGCGGATGGAACCATGATGGCACCAAGATGAGGACAGCACTTACACT  
CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT  
GTACTTGGAATGAACAGTGAGGGATACTTGTACACCTCGGAACCTTTTACACCTGAGTGCA  
AATTCAAAGAATCAGTGTTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAG  
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA  
CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT  
ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC  
AAGAGCAGAAGTGCTCTGTGGCTGTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC  
**GTAG**CCAGTGAGGGCAAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT  
TCTTCTAGCAGTCCTTCACCCAAAAGTTCAAATTTGTGAGTGACATTTACCAAACAAACAGG  
CAGAGTTCACTATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

**FIGURE 308**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIHQKQAREREKSNACKCVSSPSKGKTSCDKNKLNVFSRVKLFSGSKRRRRRP  
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA  
MNSEGILYTSSELTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGHNKEGEIMKGNHVK  
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKRSRVSGVLNGGKSMHNEST

**N-glycosylation site.**

amino acids 242-246

**Glycosaminoglycan attachment site.**

amino acids 165-169, 218-222

**Tyrosine kinase phosphorylation site.**

amino acids 93-100

**N-myristoylation site.**

amino acids 87-93, 231-237

**ATP/GTP-binding site motif A (P-loop).**

amino acids 231-239

**HBGF/FGF family proteins**

amino acids 78-94, 102-153

**FIGURE 309**

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG  
 ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG  
 CAACCTGGATATTCTGAGACATATTTTGGGGGGATTTCAGTGAAAAAGTGGGGGATCCCTT  
 CCATTTAGAGTGTAGCAAAGGAAAAACACCAAGGTTGGGTTCTTCTCTGACATTGGCAGTG  
 CCCAGTAGGGGTGGGATGAGCGAATATTTCCCAAAGCTAAAGTCCACACCCTGTAGATTAC  
 AAGAGTGGATTGTGGCAGGAGTGTGCCCCAAAATACAGTGGAAGGTGCCTGAAGATATTTAA  
 ACCACGTCTTGAAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTG  
 GAGAGGAGGGAAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG  
 AGTACATAGGCTGTGGATCTGGTGGAGCCAGCACTGGGGCCACGGGTGGTAACTGGCTGCT  
 GTGGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCCTGTGGGTGGGGCAG  
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCCAG  
 CGCGCTCCGGGCGCCTGCCGTTTGGGGGTGTCTCCTCCGGGGCGCT**ATG**CGGGCGCTGGC  
 CAGTAGCCTGATCCGGCAGAAGCGGGAGTCCGCGAGCCCCGGGGCAGCCGGCCGGTGTGG  
 CGCAGCGGCGGTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCTG  
 CTGTCCAAGGTGCGACTGTGCGGGGGGCGGCCCGCGCGCCGACCGCGGCCCGGAGCCTCA  
 GCTCAAAGGCATCGTCACCAAAGTGTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCG  
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAGCTCCTTCACCCACTTCAACCTGATCCCT  
 GTGGGCCTCCGTGTGGTCAACCATCCAGAGCGCCAAGCTGGGTCACTACATGCCATGAATGC  
 TGAGGGACTGCTCTACAGTTCGCCGATTTACAGCTGAGTGTGCTTTAAGGAGTGTGTCT  
 TTGAGAATTACTACGTCTGTACGCCTCTGCTCTCTACCGCCAGCGTCGTTCTGGCCGGGCC  
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTCATGAAGGAAACCGAGTTAAGAAGACCAA  
 GGCAGCTGCCCACTTTCTGCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC  
 ACAGTGTCCCCGAGGCCTCCCTTCCAGTCCCCCTGCCCC**TGA**AATGTAGTCCCTGGACTG  
 GAGGTTCCCTGCACTCCCACTGAGCCAGCCACCACCACAACCTGT

## **FIGURE 310**

MAALASSLIRQKREVREPGGSRFPVSAQRRVCPRGTSKSLCQKQLLILLISKVRLCGGRPARPDR  
GPEPQLKGIIVTKLFCRQGFYLANPDGSIQGTPEDTSSFTHTFNLI PVGLRVVTIQSAKLGHY  
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR  
VKKTAAAHLPLKLEVAMYQEPSSLHSVPEASPPSPAP

### **Tyrosine kinase phosphorylation site:**

amino acids 199-207

### **N-myristoylation sites:**

amino acids 54-60, 89-95, 131-137

### **HBGF/FGF family signature:**

amino acids 131-155

**FIGURE 311**

**ATG**GCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG  
GGACCGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACG  
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG  
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT  
GCAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT  
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT  
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT  
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG  
AATCTGGTAGACCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA  
GTAAAGAAAACCAACCAGCAGCTCATTTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG  
AGAACCATCTTTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA  
GCACAAGTGCGTCTGCAATAATGAATGGAGGCAAACCAAGTCAACAAGAGTAAGACAACA**TAG**

**FIGURE 312**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWRPSASRRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLR  
RQDPQLKGIVTRLYCRQGYLQMHPDGDGTDKDDSTNSTLFNLIPVGLRVVAIQGVKTGLY  
IAMNGEGYLYPSELFTECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR  
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSSTT

**N-glycosylation site.**

amino acids 100-104, 242-246

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 28-32, 29-33

**Tyrosine kinase phosphorylation site.**

amino acids 199-207

**N-myristoylation site.**

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

**HBGF/FGF family proteins.**

amino acids 104-155, 171-198





**FIGURE 314**

MLNKMTLHPQQIMIGPRFNRLFDPLLVVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC  
 VRKNLREVDPGISTNTRLLNLHENQIQIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
 NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPYESIPSYAFNRIPSLRRLDLGELKRLS  
 YISEGAFEGLSNRLYNLAMCNLREIPNLTPLIKLDLDELDSGNHLSAIRPGSFQGLMHLQKL  
 WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNDIL  
 WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE  
 LKCRASTSLTSVSWITPNGTVMTHGAYKVRIVLSDGTNLNFTNVTVQDTGMYTCMVNSNSVGN  
 TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTDNNVGPTPVVDWETTNVTTSLTPQ  
 STRSTEKTFITPVTDINSIGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN  
 HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHNYSYKSPFNHTTTVTNTINSIHSS  
 VHEPLLIRMNSKDNVQETQI

**Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,  
 434-438, 442-446, 488-492, 606-610

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
 391-397, 422-428, 433-439, 531-537

**FIGURE 315**

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGGGGCGGGCTCCCGCCCGGCACAT  
 GGCTGCAGCCACCTCGCGCGCACCCTGAGGCGCGCGCCAGCTCGCCCGAGGTCCGTGCGGA  
 GGGCGCCGGCGCCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC  
 GGC**ATG**TCCCTCCTCCTTCTCCTCTTGCTAGTTTCTACTATGTTGGAACCTTGGGGACTCA  
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGC  
 TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCATAATGAAGGGAACCAAAAA  
 GTGGTGATCACTTACTCCAGTCGTCTGTCTACAATAAATTGACTGAGGAACAGAAGGGCCG  
 AGTGGCCTTTTGCTTCCAATTTCTGGCAGGAGATGCCTCCTTGCAAGATTGAACCTCTGAAGC  
 CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTACAGGGCGCTACGTGTGGAGCCAT  
 GTCATCTTTAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC  
 AGAAGGAAGTGACCTGACCTTGACAGTGTGAGTCATCCTCTGGCACAGAGCCCATTTGTGTATT  
 ACTGGCAGCGAATCCGAGAGAAAAGGGAGAGGATGAACGTCTGCCTCCCAAACTTAGGATT  
 GACTACAACCACCTGGACAGGTTCTGCTGCAGAACTTTACCATGTCTACTCTGGACTGTA  
 CCAGTGACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGGCAGTAAGTGTACAGT  
 ATGTACAAAGCATCGGCATGTTTGCAGGAGCAGTGACAGGCATAGTGCTGGAGCCCTGCTG  
 ATTTTCTCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA  
 GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCT  
 CCTCTTCTCAGGCTCTCGAGCTCACGCTCTGGTTCTTCTCCACTCGCTCCACAGCAAAAT  
 AGTGCCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCACAGCCAGGGCTGGCCAC  
 CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATG  
 CTAATCTGACCAAGCAGAAACACACCCAGCATGATCCCCAGCCAGAGCAGAGCCCTTCCAA  
 ACGGTC**TGA**ATTACAATGGACTTGACTCCCACGCTTTCCTAGGAGTCAGGGTCTTTGGACTC  
 TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCTCTAAGTAGCA  
 GTGAGCATTGCACGGAACAGATTAGATGAGCATTTTTCTTATACAATACCAACAAGCAAA  
 AGGATGTAAGCTGATTCATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG  
 AAAGCAGGAGTCCAAATCTATTTGTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG  
 AGGTGAATATACCTAAAACCTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTACAATT  
 TTCAAGAGGAAATGGGATGCTGTTTGTAAATTTTCTATGCATTTCTGCAAACTTATTGGATT  
 ATTAGTTATTAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC  
 TGAGCTAACCACCTTCTAAGAACTCCAAAAAGGAAACATGTGTCTCTATTTCTGACTTAAC  
 TTCATTTGTATAGGTTTGGATATTAAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA  
 AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCAAAATAAC  
 TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGACTTTCCATCTTCATGATGTT  
 ATGAGGATTGTTGACAAACATTAGAAATATATAATGGACAAATTTGTGATTTCCCTCAAAT  
 CAGATGCCTCTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAAAATACAACATGTCATT  
 TATCAACGTCCTTAGAAAGATTCTTCTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATTA  
 CCCAACATACCATTTAGTCTCTTCTTCTGAGAAAATGTGAAACCAGAATTGCAAGACTGG  
 GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA  
 TGGTGCCAGGCACCTGTAGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC  
 ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

**FIGURE 316**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLVSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV  
VITYSSRHVYNNLTEEQGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV  
ILKVLVRPSKPKCELEGELTEGSDTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID  
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI  
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS  
ASRSQRTLSTDAAPQPLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 232-251

[illegible]

**FIGURE 318**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLCFVLLCGVVDFARSLSITTPPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPA  
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK  
APGVANKKIHVLVLVKPSGARCXYVDGSEEIGSDFKIKCEPKESLPLQYEWQKLSDSQKMPT  
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQCLLRNLNVPPSNKAGLIAGAIIGTLL  
ALALIGLIIFCCRKKRREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM  
EGYSKTQYNQVPSSEDFERTPQSPPTLPPAKFKYPYKTDGITVV

**Signal sequence.**

amino acids 1-19

**Transmembrane domain:**

amino acids 236-257

**N-glycosylation sites.**

amino acids 106-110, 201-205, 298-302

**Tyrosine kinase phosphorylation sites.**

amino acids 31-39, 78-85, 262-270

**N-myristoylation sites.**

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,  
245-251, 296-302

**Myelin P0 protein.**

amino acids 96-125

**FIGURE 319**

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGA  
 ATGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACCAGCTGCCTCCAGGCAGCCAGCC  
 CTCAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGC  
 CAATTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG  
 AGAGATGAAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTC  
 CTTTGCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCTGGGTTTTACCCTG  
 CTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGT  
 GAAGGGGGTGTTCCTCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG  
 CTCAGGATAACATCAGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGAT  
 GCTGAGAGCTGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAAATGTTTTCAAAAA  
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACT  
 TTGTTCTCATCGTGTCACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC  
 AGTGACACAGGCGGTTTCTGCTATTCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC  
 TCTGACCAAAGCCCTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATTTACAAGC  
 TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTGTTCCTGTGTCATTTC  
 AACAGTCTCCCTTCCTATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATT  
 TTGGCCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG  
 GTGCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTGTATTTATTACAACCTCTATTT  
 AATTAATGTCAGTATTTCAACTGAAGTCTATTTATTTGTGAGACTGTAAGTTACATGAAGG  
 CAGCAGAATATTGTGCCCCATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGCAG  
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT  
 GTTAAAAAACAGAGAGGGATGCTTGGATGTAAACTGAACTTCAGAGCATGAAAATCACACT  
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGTAAGTGATCTGTTTGAAG  
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCTCAATAAACATTTTCATT  
 TCCACCCCACTCGCCAGCTCACCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTT  
 TATCCTAGTCATTCTTCCCTAATCTTCCACTGAGTGTCAAGCTGACCTTGCTGATGGTGAC  
 ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCCTGCTAATAAAGACAACATAA  
 CTCCAAAAAAAAAAAAAAAAAAAAAAAA

320/330

### **FIGURE 320**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002  
><subunit 1 of 1, 206 aa, 1 stop  
><MW: 23799, pI: 9.12, NX(S/T): 3  
MNFQQRLQSLWTLARPFCPPLLATASQMQMVVLPCLGFTLLLSQVSGAQGQEFHFGPCQVK  
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNH  
HNRTVEVRTLKSFSSTLANNEFVLIVSQLQPSQENEMFSIRDSAHRRLFFRAFKQLDVEAAL  
TKALGEVDILLTWMQKFYKL

#### **Signal sequence:**

amino acids 1-42

#### **N-glycosylation sites.**

amino acids 85-89, 99-103, 126-130



**FIGURE 321**

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTTCCCTTTGGCTC  
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTT  
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG  
ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGGAGACTCTGCAGATCATTAAGCCCTTA  
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAGGATCA  
TCAGGAGCCAAACCCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA  
TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC  
AATGCCACCAGAGTCATCCATGACAACATATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA  
ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT  
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT  
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGACGCTGAAAGTCC  
CACTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT  
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAGGGCTGCCTT  
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT  
GTAGTACACATTGTAAGTGGTGTCTTCTGAATAAATTCATATTTTACCTATGA

322/330

## **FIGURE 322**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFFNVITLST  
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ  
RQCHCRQEATNATRVIHNDNYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

### **Signal sequence:**

amino acids 1-18

### **N-glycosylation sites.**

amino acids 56-60, 135-139

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 102-106

### **N-myristoylation site.**

amino acids 24-30

### **Actinin-type actin-binding domain signature 1.**

amino acids 159-169

**FIGURE 323**

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG  
AACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT  
AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACATGCACCTC  
GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACCATGTTGGGGGCGGCCT  
CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCA  
ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC  
AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC  
CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA  
TGAGCAGAAGATACCTCTGCATGGATTTAGAGGCAACATTTTTGGATCACACTATTTGAC  
CCGGAGAAGTGCAGGTTCCAACACCAGACGCTGGAACAGGGTACGACGCTACCACTCTCC  
TCAGTATCACTTCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCTGCCAGGCATGAACC  
CACCCCGTACTCCAGTTCCTGTCCCGAGGAACGAGATCCCCTAATTCACTTCAACACC  
CCCATACCACGGCGGCACACCCGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGT  
GCTGAAGCCCCGGGCCCCGATGACCCCGGCCCCGGCCTCCTGTTACAGGAGCTCCCGAGCG  
CCGAGGACAACAGCCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTGAGTGAAC  
ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGTTCG  
CTGG

**FIGURE 324**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGHVD  
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGY  
DVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQLSRNEIPLIHFNTPIPRRHTRSAEDDSE  
RDPLNLVKPRARMTAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTGPEGCRPFA  
KFI

**Important features of the protein:****Signal peptide:**

amino acids 1-24

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 175-179

**N-myristoylation site.**

amino acids 33-39, 100-106, 225-231, 229-235

**HBGF/FGF family proteins**

amino acids 73-124

**FIGURE 325**

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**  
 GGCTGTCTCTGGGGTCTGGCTCTGCCCCTTTCTTCTTCTGCTGGGAGGTTGGGGTCTCTGG  
 GAGCTCTGCAGGCCCCAGCACCCGAGAGCAGACACTGCGATGACAACGGACGACACAGAAG  
 TGCCCGCTATGACTCTAGCACCGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG  
 ACCTCTTCTAGGGCCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA  
 GAGAATTTCCCTGCAAGAGAGACCAGGAGTTTCACAAAAACATCTCCCAACTTCATGGTGC  
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC  
 ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCCTTGCACCGA  
 TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA  
 CAGAAGCTAAGGGCCTGTCTCAGAGAGCAGTGCCCTCTTCCGACGGCCCCCATCCAGTCATC  
 ACCCCGTACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATACCCCC  
 GTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATACCCCCGTAT  
 GGTCCCCGGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTGACTGTCACAAACATCGAG  
 GTTATTAATTGCAGCATCACAGAAATAGAAACAACAACTTCAGCATCCCTGGGGCCTCAGA  
 CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACCAGCTCTGC  
 CTGACTCCACTGAAGCAAACACACATCACTGAGGTCACAGCCTCTGCCGAGACCCTGTCC  
 ACAGCCGGCACACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA  
 CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCTCAGTGAGGCTCTGGTCA  
 CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC  
 AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGAGAGTGGGCAAAACAACCTT  
 CTTTGCTGGGAGCTCTGCTTCTCTACAGCCCCCTCGGAAGCCGCCCTCAAGAACTTCACCC  
 CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACAGCAGGGACCCCT  
 CTTCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA  
 GATCACAACCTCAGCGAAGACCAGATGAAGCCCCAACAGCCACGCCACGACTGCCCGGAC  
 GAGGCCGACCACAGAG**TGAG**TGCAGGTGAAAATGGAGTTTCTCTCTCTGCGGCTGAGTG  
 TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC  
 CGGAACTCCACGCCACGCGCCTCACTTCCAGGTCTCCTTACTGCGTGTGAGGAGGCTA  
 ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCTAGCCTG  
 GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG  
 AAGGGCAGCATGTCCAAGCCCCAATCCCCAGATGTGGCAACAGGACCTCGCTCACATCCAC  
 CGGAGTGTATGTATGGGGAGGGGCTTCACTGTTCAGAGGTGCTTGGACTCACCTTGG  
 CACATGTTCTGTGTTTCAGTAAAGAGAGACCTGATCACCATCTGTGTGCTTCCATCTGCA  
 TTAATAATTCACTCAGTGTGGCCCAAAAAA

**FIGURE 326**

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAHALETQTL  
 ETSSRASTPAGPIPEAETRGAKRISPARETRSF TKTS PNF MVLIATSVETSAASGSPEGAGM  
 TTVQTIITGSDPEEAI FDTLCTDD SSEEAKLTMDILTLAHTSTEAKGLSSESSASSD GPHPV  
 ITPSRASESSASSD GPHPVITPSRASESSASSD GPHPVITPSWSPGSDVTL LAEALVTVTNI  
 EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL  
 STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTL SGALVTVSRNPLEETSALS VETPSY  
 VKVSGAAPVSI EAGSAVGKTTSFAGSSASSYSPSEAALKNFPTSETPTMDIATKGFPPTS RD  
 PLPSVPPTTTN SSRGTNSTLAKITTS AKTTMKPQQPRPRLPGRGRPQT

**N-glycosylation sites:**

amino acids 252-256, 445-449, 451-455

**cAMP-and cGMP-dependent protein kinase phosphorylation site.**

amino acids 84-90

**Casein kinase II phosphorylation sites.**

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,  
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,  
 404-408, 414-418, 431-435

**N-myristoylation sites.**

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-  
 320, 349-355, 386-392, 397-403, 449-455

**ATP/GTP-binding site motif A (P-loop).**

amino acids 385-393

**FIGURE 327**

GCGGAGCATCCGCTGCGGTCTCTGCGGAGACCCCCGCGCGGATTGCGCGGTCTTCCCCGCGG  
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCGGGGTCTCTCGACGCCA  
 GAGAGAAATCTCATCATCTGTGTCAGCCTTCTTAAAGCAAACTAAGACCAGAGGGAGGATTAT  
 CCTTGACCTTTGAAGACCAAACCTAACTGAAATTTAAATGTTCTTTCGCGGGGAGAAGGGAG  
 CTTGACTTACACTTTGGTAATAATTTGCTTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT  
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCTATGACATCCAGTCATCTCTTTCTAAGGGAATC  
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTTCTGCTGTTCAAC  
 AAAAAACATATCAGGGGACAAAGCATGTAACCTGATGATCTTCGACACTCGAAAAACAGCTA  
 GACAACCCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA  
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG  
 CCAAGAGTTACCCAGGAAGATTCTCTTACATGGCCAATTTTCAAGCAGTCACCTCCC  
 TAGCCCATCATCACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCT  
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA  
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAAATTTTCTCTGATCAAGAAA  
 TAGTCATCTGCTGCTGAAATGTGAGTGCGCTCCAGCTACGGTGGCAGTTGCTTCTCCA  
 CATACCACCTCGGCTACTCCAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACC  
 TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC  
 AGCCTCCCACGACCCCTCATTTCTACAGTTTTTACACGGGCTCGGCTACACTCCAAGCAATG  
 GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGAAGCTCGAAAGGCAGCTTAGA  
 AACCATACCGTTTACAGAAATCTCCAACCTTAACCTTGAACACAGGGAATGTGTATAACCCTA  
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACCTGCTTCTGGGAAGGT  
 AGGGAGGCCAGTCCAGGCAGTTCTTCCCAGGGCAGTGTTCAGAAAATCAGTACGGCCTTCC  
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTCTGCTGGTGATAGGCC  
 TCGTCTCTCTGGGTAGAATCCTTTCGGAATCACTCCGAGGAAACGTTACTCAAGACTGGAT  
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT  
 TAGTAACCAGAAGCCCAAATGCAATGAGTTTCTGCTGACTTGTCTAGTCTTAGCAGGAGGTTG  
 TATTTTGAAGACAGGAAAATGCCCTTCTGCTTTCCTTTTTTTTTTTGGAGACAGAGTCTT  
 GCTCTGTTGCCAGGCTGGAGTGAGTAGCACGATCTCGGCTCTCACCGCACCTCCGTCTC  
 CTGGGTTCAAGCGATTCTCTGCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA  
 CCACACCTGGGTGATTTTTGTATTTTAGTAGAGACGGGGTTTACCATTGTTGGTCAGGCTG  
 GTCTCAAACCTCTGACCTAGTGATCCACCCTCCTCGGCTCCCAAAGTGCTGGGATTACAGG  
 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTGGTTTTTGAAGAAGATGAAGTG  
 GGAACCAATTAGGTAATTTGGGTAATCTGTCTCTAAAATATAGCTAAAAACAAAGCTCT  
 ATGTAAAGTAATAAAGTATAATGGCATATAAATTTCAAATTTCAACTGGCTTTTATGCAAA  
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTCTTGGTTCCAGATAAAATCAAC  
 TGTTTATATCAATTTCTAATGGATTGCTTTCTTTTATATGGATTCTTTTAAACCTATT  
 CCAGATGTAGTTCCTTCCAATTAATATTTGAATAAATCTTTTGTACTCAA

60  
 70  
 80  
 90  
 100  
 110  
 120  
 130  
 140  
 150  
 160  
 170  
 180  
 190  
 200  
 210  
 220  
 230  
 240  
 250  
 260  
 270  
 280  
 290  
 300  
 310  
 320  
 330

**FIGURE 328**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410

><subunit 1 of 1, 431 aa, 1 stop

><MW: 46810, pI: 6.45, NX(S/T): 6

MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEFPVYTSTQED  
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP  
SLTRNLPSEQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF  
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL  
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPPTLISTVFTRAAATLQAMATTAVLTTTFQAP  
TDSKGSLETIPFTEISNLTLTNGVNYNPTALSMNSVESSTMNKTASWEGREASPGSSSQGSV  
PENQYGLPFEKWLLIGSLLFGVLFVLVIGLVLLGRILSES LRKRYSRLDYLINGIYVDI

**Signal sequence.**

amino acids 1-25

**Transmembrane domain.**

amino acids 384-405

**N-glycosylation sites.**

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 415-419

**Tyrosine kinase phosphorylation site.**

amino acids 50-57

**N-myristoylation sites.**

amino acids 4-10, 48-54, 315-321



**FIGURE 329**

CTCCCCAGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCTCTGCTATGGGGTTGCGCTGCTGT  
 CCCAGGTTATGAAGCCCTGGAGGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT  
 CCCGTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGAGGAAGGGT  
 GGGATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAGGCCAGGAGACAAT  
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCCTGTGGA  
 ACCTCACCCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG  
 TCTTTACTGATCTCTCTGTTCGTCTTTCCAGGACCCCTGCTGTCTCTCCCTCCCTTCTCCCAC  
 CTTCCAGCCTCTGGCTACAACACGCCTGCAGCCCAAGGCAAAAGCTCAGCAAAACCCAGCCCC  
 CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG  
 GCTGAGGCCCTCCATTGGCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC  
 AGGAACCTCTCCTCACCCAGCGCTCTCTCTCTGAGGAGCTCCCGCCCCCATGCAGC  
 TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG  
 GTGTCCATCCCGATGGTCCGCATCTGCCCCAGTCTGCTGTGCTGAGCCCTCTGTGTCAGC  
 CGCAGGCCCTGATCGCCTTCTGAGCCACCTGCTCTGTGGAGAAAGGCTCAACACAGGCCA  
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCAGCCTTGACTCGGAGGAAAAGGAAGCC  
 CTTTCCAGGCCCTGAGGGGACGTGATCTCGATGCCTCCCTCCACACATCTGAGGAGGA  
 GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCTGGCCAGGCCAGCAGT  
 GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCCACCTCAGCCTCAGAG  
 TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCCTCCCCAGGCTCTCTCTTGCATGTTCCA  
 GCCTGACCTAGAAGCGTTTGTGAGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTG  
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCTCA  
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC  
 CTCATGCCCAGTGTGCGACCCCTGCCTTCCCTCCCACTCCAGACCCACCTTGTCTTCCCTCCC  
 TGGCGTCTCTCAGACTTAGTCCACGGTCTCTCTGCATCAGCTGGTGTATGAAGAGGAGCATGCT  
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGGCCCTCAGGAAGCCT  
 GTGAAAAACGTGATTCTTGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG  
 GACTCTGAATTCTAACAATGCCAGTGACTGTCGCACTTGAGTTTGAAGGCCAGTGGGCCCTG  
 ATGAACGCTCACACCCCTTCAGCTTAGAGCTGCATTTGGGCTGTGACGCTCCACCTGCC  
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCTGAGGCCTGCTAAG  
 TCCAGGCCCTTGGTCAGGTGACATTCGAGGATAAGCCAGGACCGGCACAGAAGTGG  
 TTGCCCTTNNCATTGTGCCCTCCCTGGNCCATGCCTTCTGGCTTTGGAAAAAATGATGAAGA  
 AAACCTTGGCTCCTTCTCTGTCTGGAAGGGTTACTTGCCTATGGGTCTGCTGGCTAGAGA  
 GAAAAGTAGAAAACAGAGATGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG  
 ATACCTGAAGGTGACTCCGAGTCCAGCCCTGGAGAGAGGGTTCGGGGTGGTGGTAAGTA  
 GCACAACTACTATTTTCTTTTCCATTATTATGTGTTTTTAAGACAGAATCTCGTGCT  
 GCTGCCAGGCTGGAGTGCAGTGGCAGCATCTGCAAACTCCGCCCTCTGGGTTCAGTGATT  
 CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCCACCACACCTGGCTAATT  
 TTTGACTTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGTCTGAACTCCTGAC  
 CTCAAATGAGCCTCCTGCTTCACTCTCCCAATTGCCGGGATTACAGGCATGAGCCACTGTG  
 TGTGCCCTATTTCTTTAAAAAGTGAAATTAAGAGTTGTTTCACTATGCAAACTTGGAAG  
 ATGGAGGAGAAAAAGAAAAGGAAGAAAAAATGTCAACCATAGTCTACCCAGAGACTATCAT  
 TATTTCTGTTTTGTTGACTTCTTCCACTCTTTTCTTCTTACATAATTTGCCGGTGTCTT  
 TTTACAGGAACAATTATCTGTATATACAACCTTGTATCCTGCCTTTTCCACCTTATCGTTCC  
 ATCACTTTATTCAGCACTTCTGTGTTTTACAGACCTTTTATATAAATAAATGTTTCATCA  
 GCTGCATAAAAAAAAAAAAAA

**FIGURE 330**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS  
GTIYAE EEGQETMKGRVSIRDSRQELSLIVTLWNLTIQDAGEYWCGVEKRGPD E S L L I S L F V  
FPGPCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGTGAEAPPLPG  
TSQYGHERTSQYTGTSPHPATSPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSI PMVRI  
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAE E K E A P S Q A P E G D  
VISMPLHTSEEELGFSKFVSA

**Important features:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 248-269

**N-glycosylation site.**

amino acids 96-99

**Fibrinogen beta and gamma chains C-terminal domain.**

amino acids 104-113

**Ig like V-type domain:**

amino acids 13-128